28;

218 117

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229

513

393 198 453

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289

562

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616

372 199

; Vos. Query Match 13.4%; Score 302.5; DB 2; Length 799; Best Local Similarity 24.0%; Pred. No. 6.5e-12; Indels 265; Gaps byroly Matches 150; Conservative 57; Mismatches 152; Indels 265; Gaps	OV 18 GLYGOGOVVAVADTGLDTGRNDSSNHEAFRGXITALYALGRTINN	171	Qy 64 DPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQA	VAANGLIKGVAPDANLLAYR	QY 118 WNAGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDWTVLFAAGNBGPNSGTISAPGTAKN	D-WAMAEGVVAVTSNGNSGPNNWTVGSPC	Oy 178 AITVGAT	VGATRLPYNKYKASVFTSD	Oy 195	394 FEGVDVEGKIALIVRGEIPFVEKÄENA	199	454	OY 230 RSSLAPDSSFWANINSXAYMGGTSMATFILAGNVALLKEHFIKNKALIFKFSLIAAALLI 	290 AGATDVGLGYPSGDQGWGRVTLDXSLNVAYVNEATALAT	:: 563 NTAENLVD	Qy 329GQKATYSFQAQ-AGKPLKISLVWTDAPGSTTASYTLVNDLDLVIT	DD 617 BROHFTIHNLSNKRKTYQFDVQFAGNPDGIKVKTSKNLRVQPGKT	Qy 373 APNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYTIEV	Db 662QKINFNVQVDARKLDPGY-YEGTIIVSDGSQTVEVPTILFVSEPDYFKVTTFDLDI	Qy 416QAYNVPSGPQRFSLAI 431	Db 717 DENGVLFGSAY-LPNGAEEFGLWI 739	RESULT 8 S1890 Serine proteinase (EC 3.4.21) precursor, extracellular - Xanthomonas conjugation serine proteinase and serine proteinase campestris pv. campestris C.5pecies: Xanthomonas campestris pv. campestris C.5pecies: X.N.; Tangy, J.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J. Mol. Genet. 220, 433.440, 1990 A; Reference number: \$11890; MUID: 90251253; PRID: 187155 A; Residues: 1-1890 and the structure of the
Platteeuw, C.; Siezen, R.J.; ermostable serine protease.	eference number: Z20481; MUID:96355370; PMID:8702780 ccession: T28159	tatus: prelimin olecule type: D	A; Residues: 1-1398 < VOO> A; Cross-references: EMBL: US5835; NID:g1556462; PID:g1556463; PIDN:AAB09761.1	xperimental source: DSM3 enetics:	A;Gene: pis C;Keywords: hydrolase; serine proteinase	Query Match 13.5%; Score 305; DB 2; Length 1398;	Conservative 37; Mismatches 1	Qy 21 GQGQYVAVADTGLDTGRNDSSWHEAFRGKITALYALGRTNNANDPN 66	Db 301 GNGYDIAYVDTDLDYDFTDEVPLGQYNVTYDVAVFSYYYGPLNYVLAEIDPNGE 354	67GHGTHYAGSVLGNALN	355 YAVFGWDGHGHHVAGTVAGYDSNNDAWDWLSMYSGEWEVFSRLYGWDYTNVTTDTVQG	85 MAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAMNAGARIHTNSWGAPVNGAYTANSR 14	Db 415 VAPGAQIMAIRVLRSDGRGSMWDIIEGWTYAATHGADVISMSLGGNAPYLDGTDPESV 472 OV 142 OVDRYVDNNINWTH.EAAGNEGDNGGTTGADGTAKNAITVGATE	473 AVDELTEKYGVVFVIAAGNEGFGINIVGSPGVATKATTVGAAAVPINVGVVVSOALGYPD 53	186NYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWA 24	Db 533 YYGFYYFPAYTNVRIAFFSSRGPRIDGEIKPNVVAPGYGIYSSLPMWIGGADF 585	SNYAQLREHFIKNRGITPKPS	Db 586MSGTSMATPHVSGVVALLISG-PKPEGIYYNPDIIKKVLESGATWLEGDPYT 636	QY 296 GLGYPSGDQGWGRVTLDKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPG 355	Db 637 GQKYTELDQGHGLVNVTKSWEILKAINGTTLPIVDHWADKSY 678	Qy 356 STTASYTLVNDLDLVITAPNGQKYVGN 382	SULT 7 3723 Butilisin-type proteinase (EC 3.4.21) vpr precursor [similarity] - Bacillus Date: 01-Dec-2000 #text_change 15-Jun-2001 Accession: Bacillus halodurans Accession: Basillus halodurans Accession: Basillus halodurans Accession: Basillus halodurans Cleic Acids Res. 28, 4317-4331, 2000 Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodu Accession: G83753

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ase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris pv. c
mes: subtilisin-related proteinase
thomonas campestris pv. campestris
-1993 #sequence_revision 07-Feb-1997 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: Xanthomonas campestris pv. campestris (C) Superfamily: subtilishin, subtilishin, subtilishin, serine proteinase (C) Superfamily: subtilishin, subtilishin, subtilishin, subtilishin, subtilishin, subtilishin, subtilishin, subtilishin, signal sequence #status predicted (SIG) (S) Superfamily: signal sequence #status predicted (SIG) (S) SIG) 
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tt. 220, 433-440, 1990
ttipurpose broad host range cloning vector and its use to characterise meter: S11890; WUID:90251253; PMID:2187155
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nces: EMBL:X51635; NID:948533; PIDN:CAA35962.1; PID:948534
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Pred. No. 7.6e-12;
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29.0%;
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Best Local Similarity
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Matches 137; Conservative 51; Mismatches 149; Indels 135; Gaps 26;	DD 607 LVITAGASTLWDYTRIGGPEGYADEVJEPSSRGPTGQGVPKEDINNIGAP 657 QY 235 PDSSFWANYNSKYARAKGGTSMATPIVAGNYAQLREHFIRMGITPKPSLIKA 286 DD 658EMASTRIDGRGYGAQPDVFGGTSEATPYTSGTLALVFGAYKEVYNTTPDPVTAKI 713 QY 287 ALLAGATDVGLGYPSGDQGMGRYTLDKSLNVANYBATALATOGYATYSFQAG 339
RESULT 9 FRESULT 9 Surface layer-associated STABLE proteinase - Staphylothermus marinus Nalternate names: hyperthermostable proteinase C; Species: Staphylothermus marinus C; Species: 120-69-2000 R; Mayr. U; Dups, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J. C; Date: 120-6, A: 73-74-4, 13-6 A; Mccession: T20900	A/Cross-references: DDB3:D38600, NID:g1536787, PIDN:BAA18912.1; PID:d1019647; PID:g2160 A/Cross-references: Extain O-7 CCOmment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens C;Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens C;Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens C;Comment: appril C;Superfamily: subtilisin homology E;1-40/Domain: signal sequence #status predicted <atp> F;1-40/Domain: signal sequence #status predicted <atp> F;1-15.465/Product: alkaline serine process I #status predicted <atp> F;1-15.465/Product: alkaline serine propeptide #status predicted <atp> F;1-15.465/Product: alkaline serine propeptide #status predicted <atp> F;1-15.467/Promain: carboxyl-terminal propeptide #status predicted <atp> F;1-15.465/Product: alkaline serine propeptide #status predicted <atp> F;1-15.40-ATP F;1-</atp></atp></atp></atp></atp></atp></atp></atp></atp></atp></atp></atp></atp></atp>

OY 264 VAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYPSGDQGWGRVTLDKSLNVAYVNEA 323	Db 322 LNGTSMATPHVAGAAALVKQKNPSWSNVQIRNH-LKNTATSLGSTNL 367
DD 448 AALIKQAAKPSATPDEVETILKNTTRSFAGSCSNCGTGVVDAAAAVNEA 495	Qy 298 GYPSG 302
Qy 324TALATGQKATYSFQAQAGKPLKISLVWIDAPGSTTASYT 362	Db 368 -YGSG 371
363 LVNDLDLVITAPNGQKYVGNDFSYPXDNNWDGRNNVENVFINAPQSGTYTIEV : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	(EC 3.4.21) A precursor - V
Db 542 MSGGTGDADLYVKLGSQPTSSSYDCRPYEGGNAEVCSFDAPQAGTYHVMI 591 Qy 416 QAYNVPSG 423	N,Alternate names: alkaline serine exoproteinase A C,Species: Vibrio alginolyticus C,Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 	; Robb, S.M.; Woods, D.R.
RESULT 11 A49778 high-alkaline serine proteinase (EC 3.4.21) precureor - Bacillus alcalophilus (strain N.alt-prate names, subtilisin homolog high-alkaline	
	5499; I s a ca t; subt
K.Yon der Laal, J.C.; Gerritse, G.; Mulleners, L.J.S.M.; van der Hoek, K.A.C.; Quax, W.J. Appl. Environ. Microbiol. 57, 901-909, 1991 Appl. Environ. Microbiol. 57, 901-909, 1991 A/Title: Cloning, characterization, and multiple chromosomal integration of a Bacillus a	C:keywords: calclum; nytotolase; setine proteinase F;1.21/Domain: signal sequence #status predicted <sig> F;22-534/Product: alkaline serine proteinase A #status predicted <mat></mat></sig>
A;Kererence number: A49778; MUID:91282483; PMID:2059048 A;Accession: A49778 A;Molecule type: DNA	F:171-374 bDmain: subclibain nomology https://www.newinch.gov/redicted F:271-273,297-229/Region: Slopecificity crevice #status predicted F:180,213,363/Active site: Asp, His, Ser #status predicted
A.Residues: 1-380 <van> A.Toross-references: GB.MA55086; NID:g142456; PIDN:AAA22212.1; PID:g142457 A.Toross-references: GB.Marca and and all a</van>	Query Match 11.7%; Score 265; DB 1; Length 534;
	65; Mismato
Klandmul, n.; Nobayashi, 1.; Nobayashi, M.; Tamamoto, M.; Nakamura, S.; Aono, K.; Horiko Biosci, Biotechnol. Biochem. 56, 1455-14460, 1992 A.Title: Molecular cloning. nucleotide secuence, and expression of the structural gene fi	QY 7 IVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAF 46
	Db 137 İVSADANQTNALWGLDRIDQRNLPLDNNYSANFDGTGVTAYVIDTGVNNAHVEF 190
A;Molecule type: DNA A;Residues: 1-195; SY, 197-380 <tak> A;Residues: 1-195; SY, 197-380 <tak> A;Gross-references: GR:N13157; NID: A311; DIDN: RAANO442 1; DID. A316333</tak></tak>	Qy 47 RGKITALY-ALGRINNANDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGL 103
A/Experimental source: Bacillus alcalophilus Vedder, ATCC 21522 (Bacillus sp. 221) C/Superfamentally: subtilisin is subtilisin homology	104 GGLPSNINTLESQAMNAGARIHTNEWGAPVNGAYTANSRQYDEYVRNNDWTVLFAAGNEG 16
C./scyworus: iyulorase; sellie plotelidae; zymogen F./1-27/Domain: signal seguence Hatatus predicted <sig> F./8-111/Domain: artivation menide detatus prodicted /DDD.</sig>	Db 249 SGVIAGVD#VAANASGPSVANMSLGGGQSVALDSAVQSAVQSG-VSFWLAAGNSN 302
Fill2-380/Product: alkaline serine proteinase #status predicted <mat> Fill2-380/Product: alkaline serine proteinase #status predicted <mat> Fill34-340/Domain: subtilisin homology <sbt> Fill3,173,326/Active site: Asp, His, Ser #status predicted</sbt></mat></mat>	QY 164 PNSGTISAPGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPG 223 ::
Query Match 11.9%; Score 269; DB 2; Length 380; Best Local Similarity 31.8%; Pred. No. 3.5e-10; Matches 97; Conservative 35; Mismatches 99; Indels 74; Gaps 14;	QY 224 TFILSARSSLAPDSSFWANYNSKYAYMGGTSWATPIVAGNVAQLREHFIKNRGITDKPSL 283 1
OY 13 AQNNYGLYQGQYVAVADIGLDIGRNDSSMHEAFRGKITALYALGRINNANDBNGHGTHV 72	QY 284 IKAALIAGATOVGLGYPEGDQGWGRVTLDKSLNVAY 319
QY 73 AGSVLGNALN-KGMAPQANLVFOSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTNSW 129	QY 320 VNEATALATGGKATYSFQAQAGKPLKISLVWTDAPGSTTASYTLVNDLDLVITAPNGGKY 379 1 :
QY 130 GAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRP 189	QY 380 VGNDFSYPYDNNWDGRNNVENVFINAPQSGTYTIEVQAYNVPSG 423 DD 487PILNAWDCRPFKYGNNETCTVSATQSGRYHVMIQGYSNYSG 527
OY 190 SFGSLADNPHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKYAY 249 DD 286DONNNRASFSOYGAGLILVAPGVAVOSTYPGSTYAS 321	RESULT 13 833407
250 MGGTSMATPIVAGNVAOLREHFIKNRGITPKPSLIKAALIAGATDVGL 2	<pre>subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39) C;Species: Bacillus sp. C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999</pre>

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probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix (strain probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix
C.Species: Aeropyrum pernix
C.Species: Ao-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C.Accession: A72647
B.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A.Reference number: A72450; MUID:99310339; PMID:10382966
A.Status: preliminary
A.Status: preliminary
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A.Status: DNA
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                                                                                                                                                                                              303
                                                                                                                                                                                                                                                                                                                                                                                                                                  420 LITGESVNLGWRLGFDYAGLVLPGLDPQGRWVSILYDTLAHGTSVA-TVLASRGNVEFNL 478
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                                                                                                                                                                                                                                                                            130 GAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRP 189
                                                                                                                                                                                                                                                                                                                                                                                                190 SFGSLADNPNHIAQFSSRGATRDG-----RIKPDVTAPGTFILSARSSLAPDSSFWANY 243
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                                           GOGOVVAVADTGLDTGRNDSSMH-EAFRGKITALYALGRT---NNANDPNGHGTHVAGSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 AVADIGLDIGRNDSSMHE-AFRGKITALYA-----
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                                                                                                   the subtilisin from the antarctid
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C;Species: Bacillus sp.
C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
C;Accession: S25835
R;Davail, S; Feller, G; Narinx, E; Gerday, C.
Gene 119, 143-144, 1992
A;Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacil
A;Reference number: S25835 MUID:93012966; PMID:1398082
A;Title: S25835
A;Molecule type: DNA
A;Residues: 1-419 cDAV>
A;Cross-references: BMBL:X6353; NID:940188; PIDN:CAA45096.1; PID:940199
C;Superfamily: subtilisin; subtilisin; homology
C;Keywords: extracellular protein; hydrolase; serine proteinase
F;11-23/Domain: signal sequence #status predicted <SIG>F;11-1419/Product: microbial serine proteinase #status predicted
F;114-19/Product: microbial serine proteinase #status predicted
F;114,184,359/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
C; Accession: $23407
R; Marinx, E.; Davall, S.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1131, 111-113, 1992
A; Title: Nucleotide and derived amino acid sequence of the subtilisin from the A; Reference number: $23407; MUID: 92256481; PMID: 1581352
A; Molecule type: DNA
A; Residues: 1-420 «NAR»
C; Genetics:
A; Gene: subl
C; Superfamily: subtilisin; subtilisin homology
C; Reywords: extracellular protein; hydrolase; serine proteinase
F; 1-23/Domain: signal sequence #status predicted «SIG»
F; A-111/Domain: signal sequence #status predicted «SIG»
F; 112-420/Product: microbial serine proteinase #status predicted «MAT»
F; 112-420/Product: microbial serine proteinase #status predicted
F; 1145, 185, 360/Active site: Asp, His, Ser #status predicted
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Best Local Similarity 30.7%
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ThrGluAsnTyrArgProSerPheGlySerIleAlaAspAsnProAsnHisIleAlaGln 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 ArgThrAsnAsnAlaSerAspProAsnGlyHisGlyThrHisValAlaGlySerValLeu 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GlyLeuTyrGlyGlnGlyGlnValValAlayalAlaAspThrGlyLeuAspThrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 GlyAsnAlaLeuAsn------LysGlyMetAlaProGlnAlaAsnLeuVal
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132
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Mismatches:
Indels:
Gaps:
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Matches:
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                                               NO.
                             LOCATION: 338...2539
IDENTIFICATION METHOD:
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                9.196-25
345.50
41.15%
29.20%
15.29%
                NAME/KEY:
                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No .
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US-09-514-340-3
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TITLE OF INVENTION: GENE BRODODING A PROTEIN HAVING ASYMMETRIC
HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE
ITS EXPRESSION PRODUCT
                                                                                                                                                                                                       2047
                                                                                                                                                                                                                                                                                                                                            TCGGCGTACGTGGTCGCCACGGGCGGCGGGGCAGACGGTCCGCACGGCCGCCGCGGTGCAG 2167
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                                                                                                                                    1958 ACGICGACCGCCACCGACCCCAAGGGCAGGCGGCCCCGGCGGGCTICIICIACGCTGGGC 2017
ATCGCCGACCCGGTCTCGGTGAGCTTCGGCGTCCAGCAGTGGCCGCACACGCGACGACGAG
                                                                                                   364
                                                                                                                                                                                                                                       -----AsnAsnValGlu 399
                                                                                                                                                                     AsnAspLeuAspLeuValIleThrAlaProAsnGlyGlnLysTyrValGlyAsnAspPhe 384
                                 GlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIle
                                                                                                   SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal
                                                                                                                                                                                              .898 CCGGTCACCAAGCAGCTGACCTACCGCAACCTCGGCACCCCAGGACGTCACGCTGAAGCTG
                                                                                                                                                                                                                                                                                                         AsnValPheIleAsnAlaProGlnSerGlyThrTyrIle-----
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ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIF: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDSPEECE 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,340
FILING DATE: 28-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
TILING DATE: January 30, 1998
ATTORNEY/AGENT INPORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REPREBRENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STRAIN: A-914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2539 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09514340 Patent No. 6361987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-721-8250
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STRANDEDNESS: double
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 PheGlnSerIleMetAspSerSerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThr 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                 ORGANISM: Streptomyces viridosporus
STRAIN: A-914
                                                                                                                                                                               ORGANISM: Streptomyces antibioticus
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
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340.50
40.93%
28.98%
15.07%
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LOCATION: 2540...2809
IDENTIFICATION METHOD:
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Best Local Similarity:
                                                                                                                                                      STRAIN: A-91
ORIGINAL SOURCE
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NAME/KEY:
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Sequence 1, Application US/09000016
Sequence No. 6143541
GENERAL INFORMATION:
APPLICANT: Akira ARISAMA et al.
APPLICANT: Akira ARISAMA et al.
TITLE OF INVENTION: HVDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE ITITLE OF INVENTION: ITS EXPRESSION PRODUCT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       1958 ACGTCGACCGCCACCGAAGGGCAAGGCGGCCCCGGCGGGCTTCTTCACGCTGGGC 2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1898 CCGGTCACCAAGCTGACCTACCGCAACCTCGGCACCCAGGACGTCACGTCACGTGAAGCTG 1957
                                                                                                                                                                                                                                                                                                                                                                           ----- 2047
                                                                                                                                                                      1838 ATCGCCGACCCGGTCTCGGTGAGCTTCGGCGTCGCAGTGGCCGCACACCGACGACGAG 1897
                                                                                                                                                                                                                                                                       347 SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal 364
                                                                                                                                                                                                                                                                                                                                                                                                          385 SerTyrProTyrAspAsnAsnTrpAspGlyArg------AsnAsnValGlu 399
                                                                                                                                                                                                                                                                                                                                         365 AsnAspLeuAspLeuVallleThrAlaProAsnGlyGlnLysTyrValGlyAsnAspPhe 384
     LeuIleLysAlaAlaLeu-----IleAlaGlyAlaThrAspValGlyLeuGlyTyr 299
                                                                       300 ProAsnGlyAspGlnGlyTrpGlyArgValThrLeuAsnLysSerLeuAsnValAlaTyr 319
                                                                                                                                                                                                        -----GlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLyBProLeuLysIle 346
                                                                                                                                                                                                                                                                                                                                                                                                                                            400 AsnValPhelleAsnAlaProGlnSerGlyThrTyrIle-----
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                                                                                                                                          320 ValAsnGluAlaThrAlaLeuAlaThrGly------
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,016
FILING DATE: January 30, 1998
CLASSIFICATION: 530
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APPLICATION NUMBER:
FILING DATE.
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBHONE: 202-721-8200
TELEBAX: 202-721-8250
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STREET: 2033 K St
CITY: Washington
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STATE: D.C.
COUNTRY: U.8
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US-09-000-016-1
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Percent Similarity: 41.15% Conservative: 54 Best Local Similarity: 29.20% Mismatches: 170 Query Match: 15.29% Indels: 96 DB: 3 Gaps: 18	US-09-985-689A-4 (1-433) x US-09-000-016-3 (1-2539)	Qy 18 GlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArg 37	Db 998 GGCTACGACGGCAAGGGCGTGAAGATCGCCGTCCTGGACACGGGTCCGACACGAGC 1054					GlyAsnAlaLeuAsnLysGlyMetAlaProGlnAlaAsnLeuVal 92	21	Qy 93 PhedlnSerIleMetAspSerSerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThr 112	122V Ancedorandelicticanosistic	acceaegececeaegecercaceargagecreege	131	r -1	uTyrValArgAsnAsnAspM	1367	Qy 164 ProAsnSerGlyThrIleSerAlaProGlyThrAlaLysAsnAlaIleThrValGlyAla 183	C -T		1481	Oy 204 PheSerSerArgG1yAlaThrArgAspG17Arg11eLy8ProAspValThrAlaPro 222	223 GlyThrPheIleLeuSerAlaargSerSerLeualaarroasserSerPheTrpAlaAsn 2	 1568 GGCGTGGACAT	rLysTyrAlaTyrMe	Db 1628 GGACCGGCCGGCTACATGACCATCTCCGGGACGTCGATGGCGACCCCGCACGTCGCGGGC 1687	rgG	Db 1688 GCGGCGCCCCTCTGAAGCAGCAG	1GlyLeuGlyTyr	17	ო ,	cecrccascagaccers 18	Qy 320 ValAsnGluAlaThrAlaLeuAlaThrGly329
Qy 358 ThralaSerTyrThrLeuValAsnaspLeuAspLeuValileThralaProAsnGlyGln 377	Oy 378 LysTyrValGlyAsnAspPheSerTyrProTyrAspAsnAsnTrpAspGlyArgAsnAsn 397	Db 1465GGGAACGAGGTTGACTACTCCTACACCGCCTACTACTACTACTACTACTACTACTACTACTACTACTA	Oy 398 ValgluAsnValPhelleAsnAlaproGlnSerGlyThrTyrIlelleGluValGlnAla 417	Db 1504 TTCGAGAAGGTCGGGTACTACAACCGGGCGGAACCTGGACGGTCAGGTCGTCAGC 1563	Qy 418 TyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432	Db 1564 TACAAGGGCGCGGCGAACTACCAGGTCGACGTCGTC 1599	RESULT 12	US-U9-U00-016-3 ; Sequence 3, Application US/0900016 ; Dat-off NO 6143441	GENERAL INFORMATION:	; APPLICANT: Akira ARISAWA et al. ; TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC ; TITLE OF INVENTION: HYDROLASE ACTUATY SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIV	; TITLE OF INVENTION: ITS EXPRESSION PRODUCT; NUMBER OF SEQUENCES: 7	CORRESPONDENCE ADDRESS: ; ADDRESSEE Wenderoth, Lind & Ponack, L.L.P. ; STREET: 203 K Street, N.W., #800		COUNTRY: U.S.A.	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb		SOFTWARE: Wordperfect 5.1 ; CURRENT APPLICATION DATA:	; APPLICATION NUMBER: US/09/000,016 ; FILING DATE: January 30, 1998	; PRICHASTICATION 330 ; PRICHASTICATION DATA: ; APPLICATION NUMBER:	FILING DATE:	NAME: Warren M. Cheek, Jr. , REGISTRATION NUMBER: 33,367	; REFERENCE/DOCKET NUMBER: ; TELECOMMUNICATION INFORMATION: . TELECOMMUNICATION 1002-071-070	TELEFAX: 202-721-8250 TELEFAX: 202-721-8250 TELEX:	; INFORMATION FOR SEQ ID NO: 3: ; SEQUENCE CHARACTERISTICS:	; LENGTH: 2539 base pairs ; TYPE: nucleic acid	STRANDEDNESS: double TOPOLOGY: linear	omic DN) ORGANISM: Streptomyces viridosporus ; HISTAIN: A-914	FEATURE: NAME/KEY: CDS TOWNSTON	; LOCATION: 3382539 ; LOCATION METHOD: E	02-04-000-016-3	Alignment Scores: 9.19e-25 Length: 2539 Pred. No.: 345.50 Matches: 132

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1111 TACACCAAGGCCTCTGGAACCAGCATGGCCACCCCGCACGTTTCGGGCGTTGGCGCGCT 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 ArgGlyAlaThrArgAspGlyArgIleLy8ProAspValThrAlaProGlyThrPheile 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 LeuserAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsnTyrAsnSerLys 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 ilelyshladjaLeuileAlaGlyAlaThrAspValGly---LeuGlyTyrProAsnGly 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaAsnLeuValPheGlnSerIleMet-----AapSerSerGlyGlyLeuGlyGlyLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProserAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAlaGlyAlaArgIleHisThr 126
                                                                                       613 TCAATAGCAGCTGGTACTGGAGCAGCAAGTAATGGCAAGTACAAGGGAATGGCTCCAGGA 672
                                                                                                                                                                                                                                                                                                                                                                     74 GlyservalLeuGly------AsnAlaLeuAsnLysGlyMetAlaProGln 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          673 GCTAAAGCTGGGGAATTAAAGGTTCTAGGTGCCAATGGTTCTGGAAGCATATCTACTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 AsnSerTrpGlyAlaProValAsnGlyAlaTyrThrAlaAsnSerArgGlnValAspGlu
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TTTGTCAATGGTAGG---AGTTATCCATACGATGACCATGGACATGGACATGGACTTGTAGCT
                                                   16 AsnIyrGlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThr
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511 -------GCTTCTCATCCAGAAAGTAAGTAAGTAGGTGGGTAGAT
                                                                                                                                                                                                                                                               54 TyralaLeuGlyArgThrAsnAsnAlaSerAspProAsnGlyHisGlyThrHisValAla
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US-09-985-689A-4 (1-433) x US-08-894-818B-6 (1-1977)
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                                                                                     ----ACCGCCTACTATGGA 1503
                                                                                                                                                                       398 ValGluAsnValPhelleAsnAlaProGlnSerGlyThrTyrIleljeGluValGlnAla 417
                               LysTyrvalGlyAsnAspPheSerTyrProTyrAspAsnAsnTrpAspGlyArgAsnAsn 397
                                                                                                                                                                                                                                                                                                 1564 TAC-----AGCGGAAGTGCAAACTATCAAGTAGATGTGGTA 1599
                                                                                                                                                                                                                                           TyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432
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ADDRESSE:
ADDRESSE:
Browdy and Neimark
STRET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: BY PC COMPATIBLE
OFFRATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
FILING DATE: 10-NOV-1996
PRICK APPLICATION NUMBER: PCT/0P96/03253
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 12-BC-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 12-BC-1995
ATTORNEY/AGENT INFORMATION:
TELEFHONE: (202) 628-5197
TELEFHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1977 basin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TAKAKURA, Hikaru
APPLICANT: TAKAKURA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: MITTA, Masanori
APPLICANT: MITTA, Masanori
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: ATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
UNDBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
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CAGGTT-----GACTACTTAC----
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Patent No. 6261822
GENERAL INFORMATION
APPLICANT: MORISHITA, Mio
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-08-894-818B-6
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Sat Apr
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March 31, 2004, 15:58:03 ; Search time 7.49423 Seconds (without alignments) 3008.498 Million cell updates/sec
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2261
1 NDVARGIVKADVAQNNYGLY........EVQAYNVPSGPQRFSLAIVH 433
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                              141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_42:*

Database :

SUMMARIES

	Description	dictyoste	P54683 dictyosteli	P29141 bacillus su	P72186 pyrococcus		bacillus	P29600 bacillus le	bacillus	bacillus	vibrio al	bacillus	bacillus	Q45670 bacillus sp	bacillus	P15926 streptococc	bacillus	bacillus		thermus a		P58099 streptococc	P29118 cephalospor		P11018 bacillus su			ratt	ğ	baci	bacillus	baci	bacillus	P00782 bacillus am
SUMMARIES	ΠD	TAGC DICDI	TAGB_DICDI	SUBV_BACSU	PLS PYRFU	EXPR XANCP	PRIM_BACSP	SUBS_BACLE	ELYA_BACAO	ELYA_BACCS	PROA_VIBAL	SUBT_BACS9	SUBB_BACLE	THES_BACSP	WPRA BACSU	SCA1_STRPY	ELYA_BACSP	SUBT_BACLI	ISP BACCS	AQLI THEAQ	TKSU_PYRKO	SCA2_STRPY	ALP_CEPAC	MS1P_HUMAN	ISP1_BACSU	MS1P_CRIGR	MS1P_MOUSE	MS1P_RAT	SUBN_BACNA			ᄓ		SUBT_BACAM
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SUBT_BACPU	THET_THEVU BPRX_BACNO	SMP1_MAGPO CUDP_METAN	ISP_PAEPO	PEPC ASPNG	YLPI_SCHPO HLY_HAL17
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on institute by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a long as experient is in no way or send an email to license@isb-sib.ch).
                                                                                       727 NWIHYVNNNNSNNNNKTSDGITKFDGIGGLDLRLVKPNQWKEESLSTGQNTSYCFTYKPS 786
                                                                                                                                   337 --QAQAGKPLK---ISLVWIDAPGSTIASYILVNDLDLVIIAPNGQKYVGNDFSYPYDN- 390
                                                                                                                                                                    187 SSSSNSGNNIPRVVATLVWTDPPSYAGAKFNLVNNLDLTMI-----YYRDNGSTIFYSNQ 841
                                               -----336
667 SNKLQPTGSLLKALMINNAQLLNGTFQLITSSSITYPSNQVFENFAGASLVQGWGAIRMS 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R InterPro; BOR003593; AAA ATPase.
R InterPro; IPR003593; AAA ATPase.
R InterPro; IPR003593; AAA ATPase.
R InterPro; IPR003593; ABC_TM_transporter.
InterPro; IPR000209; Peptidase_S8.
R InterPro; PR000209; Peptidase_S8.
R Pfam; PF000064; ABC_Transporter; I.
PR RMS; PR00703; SUBTILISIN:
R Pfam; PF00006; ABC_Transporter; I.
R PROSTIE; PS5032; AAAI TI.F; I.
R RNAST; SM00323; AAAI TI.F; I.
R RNGSITE; PS50329; ABC_TRANSPORTER_2; I.
R RNGSITE; PS00136; SUBTILASE_ASP; PALSE_NEG.
R RROSTIE; PS00136; SUBTILASE_HIS; I.
R RNGSITE; PS00136; SUBTILASE_HIS; I.
R RNGSITE; PS00136; SUBTILASE_HIS; I.
R RNGSITE; PS00136; SUBTILASE_ERR; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shaulsky G., Kuspa A., Loomis W.F.;
"A multidrug resistance transporter/serine protease gene is required
"A multidrug resistance transporter/serine protease gene is required
for prestalk specialization in Dictyostelium.";
Genes Dev. 9:1111-1122(1995).
-;- FUNCTION: Intercellular communication via tagB may mediate
integration of cellular differentiation with morphogenesis.
-;- SIMIDARITY: In the N-terminal section; belongs to peptidase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY. -!- SIMILARITY: STRONG, TO TAGC.
                                                                                                                                                                                                                                                      842 GGSSFLGLAPTQDTLNNVEGIVHNPTEPMTREMVAGTNVPMGPQNFS 889
                                                                                                                                                                                                                             391 ------NWDGRNNVENVFINAPQSGTYTIEVQAYNVPSGPQRFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagB precursor (EC 3.4.21.-).
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Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
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MEDLINE=95262903; PubMed=7744252;
                                               313 KSLNVAYVNEAT-----
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PIR, T18267, T18267.
MEROPS; SOB.UPW; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 NRGITPKPSLIKAALIAGA-----TDVGLGYPSGD-------QGWGRVTLD 312 ; ; | | | | | | | | | : : | | | | | | : :
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                                     PRESTALK-SPECIFIC PROTEIN TAGE.
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P-LKISLVWIDAPGSTTASYTLVNDLDL-----VITAPN--GOXYVGNDFSYPYDN 390
  MEDILINE SUGGAGES PLANGED STATES AND ALTHOUGH A.M. Alloni G.,

A ZEVEGO V., DETTERO M.G., BESSIERS P., Bolotin A., Borchert S.,

A ZEVEGO V., DETTERO M.G., BESSIERS P., Bolotin A., Borchert S.,

A ZEVEGO V., DETTERO M.G., DESSIERS P., BOLOTIN A., BORCHERT S.,

B DENISER R., BURSCHI C.V., Caldwell B. Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

B Denizer F., Devine K.M., Dusterhoft A., Enlich S.D., Emmerson P.T.,

B Anima K.D., Errington J., Fabret C., Ferrari E., Foulgar D.,

Rhim S.Y., Glasser P., Goffeau A., Golightly E.J., Grandi G.,

A Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Kobaysahi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,

A Medina N., Mellado R., E., Mizuno M., Moestl D., Nakai S., Noback M.,

Barro V., Pohl T.M., Pottetelle B., Rapoport G., Rey M., Reynolds S.,

Rieger M., Rivolta C., Rocha E., Schoeber M., Sadaie Y.,

Sekiguchi J., Sekneks A., Seror S.J., Serror P., Shin B.S.,

Sekiguchi J., Sekwaska A., Seror S.J., Serror P., Shin B.S.,

A Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Takeuchi A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
                                                          PRIVATLVWTDPPSYSGAKFNLVNNLDLLLLNSDDDSIITIGNSGGSLQPAGKVAQP---
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MEDLINE=92041574; PubMed=1938892;
Sloma_A., Rufo G.A. Jr., Theriault K.A., Dwyer M., Wilson S.W.,
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                                                                                               391 NWDGRNNVENVFINAPQSGTYTIEVQAYNVPSGPQRFS
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor extracellular protease vpr precursor (EC
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(BY SIMILARITY).
                                                                        Nature 330:249-256(1997).

- FUNCTION: NOT REQUIRED FOR GROWTH OR SPORULATION.
-! SUBCELLULAR LOCATION: Secreted.
-!- FUM: PROBABLY UNDERGOES C-TERMINAL PROCESSING OR PROTEOLYSIS.
-!- SIMILARITY: Belongs to peptidase family S8.
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Pfam, PF00082; Peptidase S8; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE ASP; 1.
PROSITE; PS00137; SUBTILIASE ASP; 1.
PROSITE; PS00138; SUBTILIASE ER; 1.
PROSITE; PS00138; SUBTILIASE ER; 1.
Hydrolase; Serine protease; Zymogen; Sign;
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Subrilist, BG10591; vpr.
InterPro; IPR001313; PA.
InterPro; IPR002209; Pepridase SB.
InterPro; IPR0090209; Protease_Inhib.
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EMBL, X73124, CAA51611.1, -.
EMBL, 299123, CAB15835.1, -.
PIR, A41341, A41341.
HSSP, P00782, 2SBT.
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---AKPKWSVEQIKAAIMN 565
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                                                                          291 GATDV----GLGYPSGDQGWGRVTLDKSLNVAYVNEATALATGQKATY-SFQAQAGKPLK
                                                                                                                                                     566 TAVTLKDSDGEVYPHNAQGAG-----SARIMNAIKADSLVSPGSYSYGTFLKENGNETK
                                                                                                                                                                                                                                        346 ISLVWTDAPGSTTASYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINA
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SECUENCE OF 36353 / JCM 8422;
MEDLINE=96355370; PubMed=8702780;
Voorhorst W.G.B., Eggen R.I.L., Geerling A.C.M., Platteeuw C.,
Siezen R.J., de Vos W.M.;
Isolation and characterization of the hyperthermostable serine
protease, pyrolysin, and its gene from the hyperthermophilic archaeon
Pyrococcus furiosus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: Glycosylated.
-!- MISCELLANEOUS: Thermostable; high activity at 95 degrees Celsius.
-!- SIMILARITY: Belongs to peptidase family 88.
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MEDINE=21079021; PubMed=11210516;
MEDINE=21079021; PubMed=11210516;
de Vos W.M., Voorhorst W.G.B., Dijkgraaf M., Kluskens L.D.,
Van der Oost J., Siezen R.J.;
"Purification, characterization, and molecular modeling of pyrolysin
and other extracellular thermostable serine proteases from
hyperthermophilic microorganisms.";
Meth. Enzymol. 330-393(2001).
I- FUNCTION: Has endopeptidate activity toward caseins, casein
fragments including alpha-S1-casein and synthetic peptides.
I- SIDGELLUAR LOCATION: Cell envelope associated.
I- PTM: LWM pyrolysin seems to be produced by autoproteolytic
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Wasiss R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-CCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Pyrolysin precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1398 AA
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                                                                                                                                                                                                                                                                                                                            620 NETFIIENQSSIRKSYTL----
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RAIN-GENERATION N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE C 3913 / NCPPB 528;

RAIN-ATCC 3913 / NCPPB 528;

RAIN-ATTC 3
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                                                     GLGYPSGDQGWGRVTLDKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPG 355
                              NYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGAT-----DV
                                                                                                                                                           637 GOKYTELDÓGHGLVNVTKSWEI-------LKAINGTTLPIVDHWADKSY
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Liu Y.-N., Tang J.-L., Clarke B.R., Dow J.M., Daniels M.J.;
"A multipurpose broad host range cloning vector and its use to
characterise an extracellular protease gene of Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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01-NOV-1991 (Rel. 20, Last sequence update)
01-RED-2003 (Rel. 41, Last annotation update)
Extracellular protease precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                        580 AA
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Xanthomonadaceae; Xanthomonas.
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PROSITE; PS00136; SUBTILIASE ASP; 1.
PROSITE; PS00137; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_HIS; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Complete proteome.
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InterPro; IPR007280; PPC.
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Pfam; PF04151; PPC; 1.
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MEDITIES 953882; PROMONEGA-763237;
KODAYAShI T., Hakamada Y., Adachi S., Hitomi J., Yoshimatsu T.,
Kolek, K., Kawai S., Ito S.,
Foike, K., Kawai S., Ito S.,
Purification and properties of an alkaline protease from
alkalophilic Bacillus sp. KSM-K16.";
Appl. Microbiol. Blocechhol. 43:473-481(1995).
-!- COFACTOR: Binds 2 calcium ions per subunit.
-!- SUBUNIT: Monomer.
-!- SUBUNIT: Belongs to peptidase family S8.

MEROPS; S08.010; --
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R FRINTS; PRO0723; SUBTILIASE S8; 1.

R PROSITE; PRO07136; SUBTILIASE ASP; 1.

R PROSITE; PRO0136; SUBTILIASE ASP; 1.

R PROSITE; PRO0137; SUBTILIASE SER; 1.

R PROSITE; PRO0138; SUBTILIASE SER; 1.

R PROSITE; PRO0138; SUBTILIASE SER; 1.

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   "Structure of a new alkaline serine protease (M-protease)
Bacillus sp. KSM-K16.";
Acta Crystallogr. D 51:199-206(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 KPDVTAPGTFILSARSS--LAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIK 273
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SYSTEM (BY SIMILARITY)
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SYSTEM (BY SIMILARITY)
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larity 29.0%; Pred. No. 3.3e-12;
Conservative 51; Mismatches 149; Indels 135;
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR007280; PPC.
InterPro; IPR009020; Protease_inhib.
Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF04151; PPC; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
Hydrolase; Serine Procease; Zymogen; Signal; Complete proteome.
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
M-protese (EC 3.4.21...)
Bacillus sp. (strain KSM-K16).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Yamane T., Kani T., Hatanaka T., Suzuki A., Ashida T.,
Kobayashi T., Ito S., Yamashita O.;
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EXTRACELLULAR PROTEASE
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Best Local Similarity
Matches 137; Conserv
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PRTM BACSP

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                                                                                                                                                                                                                                                                        GAPVNGAYTANSROVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRP 189
                                                                                                                                                                                                                                                                                                                                                                                    SFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKYAY 249
                                                                                                                                                                                                                                                                                                                                                                                                                    -----DONNNRASFSQYGAGL-----DIVAPGVNVQSTYP------GSTYAS 210
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-!- FUNCTION: Subtilisin is an extracellular alkaline serine protease, it catalyzes the hydrolysis of proteins and peptide anides.

-!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity for peptide bonds, and a preference for a large uncharged residue
                                                                                                                                                                                                                                                                                                                                        13 AQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNANDPNGHGTHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 MGGISMATPIVAGNVA------QLREHFIKNRGITPKPSLIKAALIAGATDVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Crystal structure of the alkaline proteinase Savinase from Bacillus lentus at 1.4-A resolution."; J. Mol. Biol. 223:427-445(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96184511; PubMed=8654411; Remerowski M.L., Pepermans H.A.M., Hilbers C.W., van de Ven F.J.M.; Remerowski M.L., Pepermans H.A.M., Hilbers C.W., van de Ven F.J.M.; Backbone dynamics of the 269-residue protease Savinase determined from 15N-NMR relaxation measurements."; Eur. J. Biochem. 235:629-640(1996).
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MEDLINE=98426039; PubMed=9753430;
Kuhn P., Knapp M., Soltis S.M., Ganshaw G., Thoene M., Bott 1
"The 0.78-A structure of a serine protease: Bacillus lentus subtilisin.";
                                                                                                              Match 11.9%; Score 269; DB 1; Length 269; Local Similarity 31.7%; Pred. No. 1e-10; les 98; Conservative 32; Mismatches 97; Indels E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
MEDLINE=92148829; PubMed=1738156;
Betzel C., Klupsch S., Papendorf G., Hastrup S., Branner S. Wilson K.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Subtilisin Savinase (EC 3.4.21.62) (Alkaline protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus lentus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1467;
                                                                                   26723 MW; 7A03C86D534A1D07 CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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InterPro; IPR000209; Protease_Inhib.
PERN009020; Peptidase_S8; I
PERN PR00021; SUBTILISIN.
PROSITE; PR00135; SUBTILISE ASP; I.
PROSITE; PS00136; SUBTILIASE_ASP; I.
PROSITE; PS00137; SUBTILIASE_ERF; I.
PROSITE; PS00138; SUBTILIASE_ERF; I.
PROSITE; PS00128; SUBTILIASE_SER; I.
PROSITE; PS00128; SUBTILIASE_SER; I.
PROSITE; PS00128; SUBTILIASE_SER; I.
PROPEP 28 112
                                                                                                                                                                                                                                                          MEDDINE=27277237; PubMed=9115441;
Martin J.R., Mulder F.A., Karimi-Nejad Y., van der Zwan J.,
Martini M., Schipper D., Boelens R.;
"The solution structure of serine protease PB92 from Bacillus
alcalophilus presents a rigid fold with a flexible substrate-binding
MEDLINE=93078250; PubMed=1447775; Sobek H., Hecht H.-J., Aehle W., Schomburg D.; Necht H.-J., Aehle W., Schomburg D.; X-ray structure determination and comparison of two crystal a variant (Ashl15Arg) of the alkaline protease from Bacillus alcalophilus refined at 1.85-A resolution."; J. Mol. Biol. 228:108-117(1992).
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EMBL; A13738; CAA01128.1; -.
PIR; A49778, A49778.
PBDB; 1AH2; 15-APR-98.
MEROPS; S08.038; -.
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               14;
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| TATSLGSTNL-- 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AQNNYGLYGOGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNANDPNGHGTHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PB92;
MEDLINE=92390330; PubMed=1518788;
van der Laan J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset O.,
Mulleners L.J.M., Dijkstra B.W.;
"Crystal structure of the high-alkaline serine protease PB92 from
Bacillus alcalophilus.";
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MEDLINE=91282483; PubMed=2059048;
van der Laan J.C., Gerritse G., Mulleners L.J.M., van der Hoek R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, characterization, and multiple chromosomal integration of Bacillus alkaline protease gene."; Appl. Brviron. Microbiol. 57:901-909(1991).
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                                                                                                                                                                                                                                                                                                                                                                                      Length 269;
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31.8%; Pred. No. 1e-10;
ive 35; Mismatches 99; Indels
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alkaline profease precursor (EC 3.4.21.-).
Bacillus alcalophilus.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
11 TaxID=1445;
                                                                                                                                                                                                                                                                                                                             26698 MW; 4D89F8778999BF8D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.75 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31...
Best 407; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                     2231
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264
268
269 AA;
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P27693;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 SFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKYAY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 MGGTSMATPIVAGNVA------QLREHFIKNRGITPKPSLIKAALIAGATDVGL 297
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REMBL; S48754; AAC60420.1; -.
REMBL; D13157; BAA02442.1; -.
REMBL; A225617; CAA01836.1; -.
REMBL; A22560; CAA01811.1; -.
REMBL; A22560; CAA01611.1; -.
REMBL; A22560; CAA01611.1; -.
REMBL; A22560; GAA01611.1; -.
REMBL; A22560; GAA01611.1; -.
REMBL; A22560; GAA0161.1; -.
REMBL; PRO0020; Protease finib.
REMPCOST: PRO0020; Protease finib.
REMBLY: PRO0021; PRO1021; SUBTILASE ASP; 1.
REMBLY: PRO0136; SUBTILASE ASP; 1.
REMBLY: PRO0138; SUBTILASE RER; 1.
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CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74;
COFACTOR: Binds 2 calcium ions per subunit (By similarity). SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
(BY SIMILARITY).
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| : | : | 367
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                                                                                                                                                                                                                                                                                                                                                                        72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 AGTIAALNNSIGVLGVAPNAELYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHVANLSL
                                                                                                                                                                                                                                                                                                                                   Gaps
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SEQUENCE FROM N.A.
STRAIN-221 / ATCC 21522 / JCM 9139 / DSM 2512;
MEDLINE-93043753; PubMed=1368952;
Takami H., Kobayashi T., Kobayashi M., Yamamoto M., Nakamura S. Aono R., Horikoshi K.;
Aono R., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aono R., Horikoshi K.;
"Molecular cloning, nucleotide sequence, and expression of the structural gene for alkaline serine protease from alkaliphilic Bacillus sp. 221."
Bacillus Sp. 220."
Biosci. Biotechnol. Biochem. 56:1455-1460(1992).
                                                                                                                                                                                                                                                                                                  Length 380;
                                                                                                                                                                                                                                                                                            Query Match
11.9%; Score 269; DB 1; Length 38(
Best Local Similarity 31.8%; Pred. No. 1.6e-10;
Matches 97; Conservative 35; Mismatches 99; Indels
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alkaline protease precursor (EC 3.4.21.-).
Bacillus clausii.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
171 TaxID=79880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Horikoshi K.;
(In) Horikoshi K. (eds.);
Microorganisms in alkaline evironments, pp.187-194, VCH,
Weinheim (1991).
                                                                                                                                                                                                                                                           38853 MW; 539EA72771B6682C CRC64;
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STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 GGLPSNLNTLFSQAWNAGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVKADVAQ----------NNY--GLYGQGQVVAVADTGEDTGRNDSSMHEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 IVSADANQTNAIWGLDRIDQRNLPLDNNYSANFDGTGVTAYVIDTGV-----NNAHVEF
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINES #3326126; PubMed=2546861;
Deane S.M., Robb F.T., Robb S.M., Woods D.R.;

"Nucleotide sequence of the Vibrio alginolyticus calcium-dependent,
"Nucleotide sequence of the Vibrio alginolyticus calcium-dependent,
Gerergent.resistent alkaline serine exoprotease A.";

Gene 76:261-288(1989).

-! SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
84E96D9C649D4226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 265; DB 1; Length 534;
Pred. No. 4.5e-10;
5; Mismatches 152; Indels 128;
                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alkaline serine exoprotease A precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_ER; 1.
PROSITE; PS00139; SUBTILASE_SER; 1.
PHOTOJASE; Zymogen; Signal.
SIGNAL 1 21
                                                                                                                                           534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR009020; Protease_inhib.
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000209; Peptidase_S8.
InterPro; IPR007280; PPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%; (26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M25499, AAA27550.1, -. The PIR, JS0173, JS0173. HSSP, Q99405, IMPT. MEROPS, S08.050, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00082; Peptidase_S8;
Pfam; PF04151; PPC; 1.
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                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                       Vibrio alginolyticus.
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363
383
384;
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  GYPSG 302
                                       368 -¥G$Ġ 371
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=663;
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                                                                                                                                           VIBAL
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MEDITE=92256481; PubMed=1581352;

MEDITE=92256481; PubMed=1581352;

Marinx E., Davall S., Feller G., Gerday C.;

Muclectide and derived amino acid sequence of the subtilisin from antarctic psychrotroph Bacillus TA39.";

Biochim. Biophys. Acta 1131:111-113(1992).

C. I- FUNCTION: Subtilisin is an extracellular alkaline serine protease, it catalyzes the hydrolysis of proteins and peptide amides.

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity for peptide bonds, and a preference for a large uncharged residue in P1. Hydrolyzes peptide amides.

C. I- COPACTOR: Blinds I calcium ion per subunit (Potential).

C. I- SUBCELLULAR LOCATION: Secreted.

C. MISCELLANEOUS: Still active at temperatures close to 0 degrees constituted in has a marked heat lability.

C. MISCELLANEOUS: Secretion of subtilisin is associated with onset of sporulation, and many mutations which block sporulation at early stages affect expression levels of subtilisin. However, subtilisin is not necessary for normal sporulation.

C. SIMILARITY: Belongs to peptidase family S8.
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                                                                     303 ADACNYS-PARVATGVTVGST-----TSTDARSSFSNWGSC-----VDVFAPG 344
                                                                                                                                                       283
                                                                                                                                                                                                    ---TDVGLGYPSG-----DQGWGRVTLDKSLNVAY 319
                                                                                                                                                                                                                                                                                                                                                               320 VNEATALATGGKATYSFQAQAGKPLKISLVWTDAPGSTTASYTLVNDLDLVITAPNGQKY 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486
PNSGTISAPGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GISGSSGQVAYYYVDVEAGQRLTVQM-------YGGSGDADLYLRF--GAK-
                                                                                                                                                   TFILSARSSLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PILNAWDCRPFKYGNNETCTVSATQSGRYHVMIQGYSNYSG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 VGNDFSYPYDNNWDGR----NNVENVFINAPOSGTYTIEVQAYNVPSG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus sp. (strain TA39).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Subtilisin precursor (EC 3.4.21.62).
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Pfam, PF00082; Peptidase S8. 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00116; SUBTILASE ASP, 1
PROSITE; PS001137; SUBTILASE ASP, 1
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PIR; S23407; S23407.
HSSP; Q99405; IMPT.
MEROPS; S08.UPA; -.
                                                                                                                                                                                                                                                                                                          284 IKAALIAGA-----
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PDB; 1ST3; 31-JAN-94.
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X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).

X-RAY CRYSTAL STRUCTUR R.J.;

X-RAY CRYSTALLOGRAPHY (1.4 ANGS CALID STRUCTUR ANG STRUCTUR S
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                                                                                                                                                                                                                                                                                                                                                                                                 128 SWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 WANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GQGQVVAVADTGLDTGRNDSSMHEAFRGKITAL--YALGRT---NNANDPNGHGTHVAGS
                                                                                                                                                                                                                                                                                                  136 GGINIAVI.Drgvnrn-----HPDLRNNVEQCKDFTVGTTYTNNSCTDRQGHGTHVAGS
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                                                                                                                                                                                                                                        Gaps
          59;
                                                                                                                                                                                                        DB 1; Length 420;
                                                                                                                                                                                                     11.7%; Score 263.5; DB 1; Length 29.0%; Pred. No. 4.1e-10; ive 46; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
Subtilisin BL (EC 3.4.21.62) (Alkaline protease),
Bacillus lentus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                         CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
AE4F121BD32B26EC CRC64;
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PROSITE; PS00138; SUBTILASE SER; 1.
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420 AA;
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Best Local Similarity
Matches 92; Conserv
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P2959;
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OXYGEN).
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11.5%; Score 259; DB 1; Length 26
Best Local Similarity 31.5%; Pred. No. 4.5e-10;
Matches 96; Conservative 34; Mismatches 101; Indels
MEROPS; S08.003; -.
InterPro; IPR000209; Peptidase S8.
Pfan; PF00082; Peptidase S8.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROGIUM-binding; 32-grucure.
Calcium-binding; 32-grucure.
CALCIER 32.
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CHARGE RELAY SYSTEM.
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CALCIUM 1.
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                                   AGTIAALNNSIGVLGVAPSAELYAVKVLGADG--RGAISSIAQGIEWAGNNGMHVANLSL 124
                                                                                                                                                             -----DONNNRASFSQYGAGL-----DIVAPGVNVQSTYP------GSTYAS 210
                                                                                                                                                                                                              AGSV -- LCNALN-KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTNSW 129
                                                                        GAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYRP 189
                                                                                                     GSP---SPSATLEQAVNSATSRGVLVVAASGNSGASS--ISYPARYANAMAVGAT---- 174
                                                                                                                                                                                             250 MGGTSMATPIVAGNVA------QLREHFIKNRGITPKPSLIKAALIAGATDVGL 297
                                                                                                                                  SFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20057863; PubMed=10588904;
Smith C.A., Toogood H.S., Baker H.M., Daniel R.M., Baker E.N.;
Smith C.A., Toogood H.S., Baker H.M., Daniel R.M., Baker E.N.;
Calcium-mediated thermostability in the subtilisin superfamily: the crystal structure of Bacillus Ak.1 protease at 1.8-A resolution.";
J. Mol. Biol. 294:1027-1040(1999).
I- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
I- SUBCELMUAR LOCATION: Secreted.
I- MISCELLANBOUS: Has a pH optimum of 8.5, a temperature optimum of 75 degrees Celsius.
I- SIMILARITY: Belongs to peptidase family 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=95085262; PubMed=7993087;
Maciver B., McHale R.H., Saul D.J., Bergquist P.L.;
"Cloning and sequencing of a serine proteinase gene from a thermophilic Bacillus species and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                          [6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thermophilic serine proteinase precursor (EC 3.4.21.-) (Ak.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease).
Bacillus sp. (strain AKI).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Appl. Environ. Microbiol. 60:3981-3988(1994).
[2]
                                                                                                                                                                                                                                                                                                                                                                401 AA.
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Interpro, IPR009020, Protease Inhib
Pfan, PR0082, Peptidase S8, I.
PRINTS, PR00723, SUBILLISIN.
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PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
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PIR; I39974; I39974.
PDB; 1DBI; 18-NOV-99.
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Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P54423; 006726; 01.34; Created) 15-DEC-1996 (Rel. 34, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 10-OCT-2003 (Rel. 37, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update) wall-associated protease precursor (EC 3.4.21.-) [Contains: Cell wall-associated polypeptides CWBP23 and CWBP52]. Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                             QNNYGLY-----GQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDP-
                                                                                                                                                       --NGHGTHVAGSVLGNALN----KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN
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                                                                                                                                                                                                                                       120 AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAFGTAKNAI
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growth, encodes a cell-wall-associated protease.";
Microbiology 142:3437-3444(1996).
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MEDLIRE=98015415; PubMed=9353931;
Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
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Microbiology 143:3305-3308(1997).
                                        58;
    Length 401;
                                     Indels
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Query Match
Best Local Similarity 31.7%; Pred. No. 1.4e-09;
Matches 85; Conservative 26; Mismatches 99
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MEDLINE=98044033; PubMed=9384377;
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MEDLINE=97158234; PubMed=9004506;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics in Stitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mosstl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Persoran E., Pulic P., Purnelle B., Porvollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Schiguchi J., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Schiguchi J., Scanlan E., Takagi T., Takahashi H., Takemaru K.,
RA Sorokin A., Tanaka T., Taraka T., Torgoroi A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RY Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
R. Tubtilis ...
Rubtilis ...
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---- SUBCELLULAR LOCATION, Cell-wall bound.
---- PTM: PROCESSED INTO CWEB23 AND CWEB22.
--- SIMILARITY: Belongs to peptidase family S8.
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Subtlist; BC01146; wpra.
InterPro; IPR000209; Peptidase S8.
InterPro; PR000209; Peptidase S8.
PROMITS; PR00023; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE ASP; FALSE_NEG.
PROSITE; PS00138; SUBTILIASE FIR; 1.
PROSITE; PS00138; SUBTILIASE ERR; 1.
Hydrolase; Serine protease; Cell wall; Zymogen; Signal;
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MEDINE=90153944; Pubmed=2406246;
Chen C.C., Cleary P.P.;
"Complete nucleotide sequence of the streptococcal C5a peptidase gene
                         PNHIAOFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKYAYMGGTSMAT
                                                                                      MDMTADFSNYGKGL-----DISAPGSDİ----PSLVP-----NGNVTYMSGTSMAT
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J. Biol. Chem. 265:3161-3167(1990).
J. Biol. Chem. 265:3161-3167(1990).
J. PUNCTION: THIS VIRULENCE FACTOR OF S.PYOGENES SPECIFICALLY CLEAVE THE HUMAN SERUM CHEMOTAXIN C5A AT LYS(68)-ASP(69) BOND NEAR ITS.
C. TERMINUS, DESTROYING ITS ABILITY TO SERVE AS A CHEMOATTRACTANT.
J. SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00746; Gram pos_anchor; 1.
Pfam; PF00725; PA; 1.
Pfam; PF00225; PA; 1.
Pfam; PF00225; PA; 1.
PROSITE; PS0047; GRAM POS_ANCHORING; 1.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00139; SUBTILASE EN; 1.
PROSITE; PS00139; SUBTILASE EN; 1.
Hydrolase; Serine protease; Cell wall; Peptidoglycan-anchor; Repeat;
                                                                                                                                                           PIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYPSGDQ----
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                                                                                                                                                                                                                                                                                            -----GWGRVTLDKSLNVA---YVN--EATALA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) C5A peptidase precursor (EC 3.4.21.-) (SCP).
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InterPro; IPR003137; PA.
InterPro; IPR00209; Peptidase_S8.
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STIMMARTES

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SUMMAKIES	DI CI	Q9AQR1	Q9AQR4	Q9AQR2	Q9AQR0	Q9AQR3	6A11660	QST9W1	COGTN7	7 Q8U0C9	6 QBRBJ2	6 Q9FBZ4	6 QBENV1	6 Q9FC06	P95684	Q9AER6	6 Q9KBJ7
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711199 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		2T 1 81 Q9AQR1	01-JUN-2001 01-JUN-2001 01-JUN-2003 Protease (Fr	Bacillus sp. Bacteria, Fi NCBI_TaxID=1	EUGUENCE FROM N.A. STRAIN=SD521, MEDLINE=20568675; PubMed=1111 Saeki K., Okuda M., Hatada Y. HOTIKOSHI K., "Novel oxidatively stable sub alkaliphilic Bacillus ssp.: e evolutionary relationships."; Biochem Blophys. Res. Commun. I. SIMILARITY: BELONGS TO PE EMBL; ABC46405; BRB1268.1; HSSP; Q45670; IDBI. G0; G0:0004289; F:subtilase a G0; G0:0004289; F:subtilase a G0; G0:0004289; F:subtilase a G0; G0:0004289; F:subtilase B EMENTY: IPRO0209; Peptidase InterPro; IPRO0209; Peptidase InterPro; IPRO0209; Peptidase InterPro; IPRO02280; Peptidase INTER PRO0723; SUBTILASE Hydrolase; Protease; Serine P NON TER 433 A33 SEQUENCE 433 AA; 45576 MW;
		RESUI O9AQF ID	888888	8888	

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Hydrolase, Protease, Serine protease.
NON TER 1 1
NON TER 433 433
SEQUENCE 433 AA, 45636 MW, 52087E
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                                                               Query Match
Best Local Simil
Matches 430; C
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A Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Horikoshi K.;
Horikoshi K.;

"Novel oxidatively stable subtilisin-like serine proteases from
a "Novel oxidatively stable subtilisin-like serine proteases from
a lkaliphilio Bacillus sep: enzymatic properties, sequences, and
evolutionary relationships ";

Biochem. Biophys Res. Commun. 279:313-319(2000).

"I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.

EMBL; ABO46402; BAB11265.1; -.

EMBL; ABO46402; BAB11265.1; -.

ROG GO:0004289; F:subtilase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

ROG GO:0004289; F:subtilase activity; IEA.

ROG GO:0004289; F:subtilase S8; 1.

R Ffam; PF004151; PPC; 1.

R PRINTS; PR00723; SUBTILIASE HIS; 1.

R PROSITE; PS00137; SUBTILIASE ESR; 1.
                                        Gaps
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             Length 433;
                                     Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Last annotation update)
            100.0%; Score 2261; DB 2;
100.0%; Pred. No. 1.8e-124;
ive 0; Mismatches 0;
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MEDLINE=20568675; PubMed=11118284;
MEDLINE=20568675; PubMed=11118284; Kob
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01-JUN-2003 (TrEMBLrel. 24,
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             Query Match
Best Local Similarity 100.
Matches 433; Conservative
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A Sacki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Sacki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
A HORINGSHI K.,
MINOVAL OXIDATIVE STABLE SUDTILISED-LIKE SETINE protesses from alkaliphilic Bacillus ssp.: enzymatic properties, sequences, and alkaliphilic Bacillus spp.: enzymatic properties, sequences, and slochem. Blophys. Res. Commun. 279:313-319(2000).
C. -- SIMILARITY: BELEONGS TO PEPTIDASE FAMILY SB.
EMBL, AB046404; BAB21267.1; -..
RSP; Q45670; IDBI.
GO: GO:0004289; F:septidase activity; IEA.
GO: GO:0004289; F:subtliase activity; IEA.
GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
RG: GO:0006508; Peptidase_SB.
R InterPro; IPR007280; Peptidase_SB.
R Pfam; PF00082; Peptidase_SB.1.
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=133779;
433
45636 MW; 52087E0A2516107F CRC64;
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                                                                                  99.6%; Score 2251; DB 2;
llarity 99.3%; Pred. No. 7.1e-124;
Conservative 1; Mismatches 2;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
Protease (Fragment).
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Blochem. Blochem. Blochys. Res. Commun. 279:313-319(2000).
                                                                                                                                                                                                                                                               DB 2; Length 434;
                                                                                                                                                                                                                                                             Query Match

89.5%; Score 2024.5; DB 2; Length
Best Local Similarity 88.5%; Pred. No. 1.3e-110;
Matches 384; Conservative 28; Mismatches 21; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR00208; Peptidase_S8.
Fram; Pr00122; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILASE.
PROSITE; PS00138; SUBTILASE_ERR; 1.
PROSITE; PS00138; SUBTILASE_ERR; 1.
Hydrolse; Protesse; Serine protesse.
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SEQÜENCE 434 AA; 45294 MW; 83517EDDB74125D2 CRC64;
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STRAIN=9860;
MEDLINE=20568675; PubMed=11118284;
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SEQUENCE FROM N.A.
MEDLINE=20568675; PubMed=11118284;
Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Horikoshi K.;
Horikoshi K.;
"Novel oxidatively stable subtilisin-like serine proteases from
alkaliphilic Bacillus ssp.: enzymatic properties, sequences, and
evolutionary relationships:";
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                                                                                                                                                                                   Length 433;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=133781;
                                                                                                                                              45587 MW; B81291A803C775AE CRC64;
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Last annotation update)
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB. EMBL; AB04640¢; BAB21269.1; -.
HSSP; PO0762; 1SUP.
GO, GO:000823; F:Peptidase activity; IEA.
GO; GO:0004289; F:Subtilase activity; IEA.
                                                                                                                                                                               99.1%; Score 2240; DB 2;
98.8%; Pred. No. 3.1e-123;
ive 4; Mismatches 1;
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                         PRINTS; PRO0723; SUBTILISIN.
PROSTIE; PS00137; SUBTILASE HIS; 1.
PROSTIE; PS00138; SUBTILASE SIR; 1.
Hydrolase; Protease; Serine protease.
NON TER 43 433
SEQUENCE 433 AA; 45587 MW; B81291
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01-JJW-2001 (TrEMBLrel. 17,
01-JJW-2001 (TrEMBLrel. 17,
01-JJW-2003 (TrEMBLrel. 24,
Protease (Fragment).
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Matches 428; Conservative
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        Pfam; PF04151; PPC; 1.
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                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                              Query Match 88.6%; Score 2002.5; DB 2; Length 639; Best Local Similarity 88.2%; Pred. No. 4.1e-109; Matches 383; Conservative 26; Mismatches 24; Indels 1;
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Itoh S., Saki K.;
"new protease.";
"new protease.";
Submitred (NOV-200) to the EMBL/GenBank/DDBJ databases.
EMBL; AB051423; BAB55674.2; -.
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000209; Peptidase_SS.
InterPro; IPR007280; PPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus sp. KSM-KP43.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=109322;
                                                                                                                                                                                                         68185 MW; 316AF6FFDBE4FF54 CRC64;
HSSP; P00782; 1SUP.

GO; GO: 0004289; F: Subtilase activity; IEA.

GO; GO: 0005608; P: Proteclysis and peptidolysis; IEA.

InterPro; IPR002209; Peptidase_S8.

InterPro; IPR007280; PPC.

Pfam; PR004151; PPC; 1.

PRINTS; PR04151; PPC; 1.

PROSITE; PS00137; SUBTILASE HIS; 1.

PROSITE; PS00138; SUBTILASE ESR; 1.
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Pfam; PF00082; Peptidase_S8; 1.
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01-OCT-2002 (TrEMBLrel. 22,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                    Query Match

88.4%; Score 1998.5; DB 2; Length 640;
Best Local Similarity 87.6%; Pred. No. 7e-109;
Matches 381; Conservative 28; Mismatches 24; Indels 1;
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C STRAINAAX4;

A Anjard C., Loomis W.F.;
Anjard C., Loomis W.F.;
Anjard C., Loomis W.F.;

Exvolution of the ABC transporters of Dictyostelium.";
Submitted (JAN-2002) to the EMBL/Genbank/DDBJ databases.

C -! SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

EMBL, AF466309; AAL74233.1; -.

R GO; GO:0006524; F:ATP binding; IEA.

R GO; GO:0004209; F:ATP-binding cassette (ABC) transporter ac

R GO; GO:0008233; F:Epptidase activity; IEA.

R GO; GO:0008239; F:subcilase activity; IEA.

R GO; GO:0006209; F:subcilase activity; IEA.

R GO; GO:0006209; F:subcilase activity; IEA.

R GO; GO:0006309; F:subcilase activity; IEA.

R GO; GO:0006303; F:ATP-APPASE.

R InterPro; IFR001140; ABC_IM_transpt.
                                                                                                                 4BBAF77E9D592C15 CRC64;
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Pfam; PF04151; PPC; 1.
PRINTS; PR00723; SUBTILLASIN.
PR051TE; PS00137; SUBTILLASE_HIS; 1.
PR051TE; PS00138; SUBTILASE_SER; 1.
SEQUENCE 640 AA; 67991 NW; 4BBAI
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Taga, a putative serine protease/ABC transporter of Dictyostelium

Taga, a putative serine protease/ABC transporter of Dictyostelium

Taga, a putative serine protease/ABC transporter of Dictyostelium

That is expressed at the onest of development and is required for the
differentiation of a subpopulation of prespore cells.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

I. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

GO; GO:00016620; C:membrane; IEA.

GO; GO:000166; F:ATP-binding; IEA.

GO; GO:000166; F:ATP-binding; IEA.

GO; GO:000166; F:ATP-binding; IEA.

GO; GO:000166; F:ATP-binding; IEA.

GO; GO:000166; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.

GO; GO:000166; F:ATP-binding; II.

GO: GO:000166; F:ATP-binding; IEA.

GO: GO:000166; F:ATP-binding; IEA.

GO: GO:000166; F:ATP-binding; IEA.

GO: GO:0001666; F:ATP-binding; IEA.

GO: GO:000166; F:ATP-binding; IEA.

GO: G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GITPKPSLIKAALIAGAT---DVGLGYPSGDQGWGRVTLDK-----SLNV-AYV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            656 VGPQPSASLVKATLINTASINVDSTLEY---SQGFGNIQLSKLITTINAQTTSLDIPSSI 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEATALA-TGOKATYSFQAQAGKPLKISLVWTDAPGSTTASYTLVNDLDLVITAPNGQKY 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGNDFSYPYDNN-------WDGRNNVENVFINAPQSGTYTIEVQAYNVPSGPORF 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWGAPVNGAYTANSRQVDEYVRNN-DMTVLFAAGNE---GPNS-GTISAPGTAKNAITVG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 APDSSFWANY-----HFIKNR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 GLYGQGQVVAVADTGLDTGR----NDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 SVLGNAL-----NKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNAGARIHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P----NHIAQ-----NHIAQ------FSSRGATRDGRIKPDVTAPGTFILSARSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0211; ABC_TRANSPORTER_1; 1.
PROSITE; PSO6931, ABC_TRANSPORTER_2; 1.
ATP-binding; Transport
SEQUENCE 1702 AA; 187103 MW; 4A67716303CB7131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.5%; Score 441.5; DB 5; 26.1%; Pred. No. 3e-17; tive 91; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 26.1% Matches 142, Conservative
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        RRANGE STATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ωp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNKLQPTGSLLKALMINNAQLLNGTFPLSSTNTNPSNAVFDTFAGANFVQGWGSLRRSEW 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 LNVAYVNEA------QQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L---YVESSGVKPKPSRWVGIGELGKDKKASNWKEYSLSTGQNVSYCFTYKPSSSGSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 LYGOGOVVAVADIGLDIGR---NDS----SMHEAFRGKIIALYALGRINNANDPNGH
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                                                                                                                                                                                                                                                                                                                                                                                                 20.6%; Score 465; DB 5; Length 1825; 26.9%; Pred. No. 1.4e-18; ive 79; Mismatches 167; Indels 17
R InterPro; IPR003439; ABC_transporter.

InterPro; IPR00209; Peptidase_S8.

Pfam; PF00064; ABC_tran; 1.

R Pfam; PF00005; ABC_tran; 1.

R PFAM; PF00005; ABC_tran; 1.

R PRINTS; PR00723; SUFILISIN.

R PRODOM; P0000006; ABC_transporter; 1.

R PROSITE; S00031; AAA; 1.

R PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

R PROSITE; PS00137; SUBFILASE_HIS; 1.

R PROSITE; PS00137; SUBFILASE_HIS; 1.

R PROSITE; PS00137; SUBFILASE_HIS; 1.

R ATP-binding; Protease; Transport.

A ATP-binding; Protease; Transport.

SEQUENCE 1825 AA; 202641 MW; E28160BC78613A3B CRC64;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
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(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
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Matches 156; Conservative
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01-MAR-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 INDYYTAAPGTSMATPHVAGIAALLLQ---AHPSWTPDKVKTALIETADIVKPDEIADIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 YPSGDOGWGRVTLDKSLNVAYVNEATALATGOKA----TYSFQAQAGKPLKISLVWTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 Y-----GAGRVNAYKAIN--YDNYAKLVFTGYVANKGSQTHQFVISGASFVTATLYWDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 NYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNAN-----DPNGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGSTTASYTLVNDLDLV1TAPNGOKYVGNDFSYPYDNNWDGRNNVENVF1NAPQSGTYTI
                                                                                                              PF1670.
Pyrococcus furiosus.
Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=Vol / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

The compilete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

R GGJ (GG):0008233; F:peptidase activity; IEA.

R GGJ (GO:0008233; F:peptidase activity; IEA.

R GGJ (GO:0008239; F:subtilase activity; IEA.

R GGJ (GO:0008239; F:subtilase activity; IEA.

R GGJ (GO:0008239; F:subtilase activity; IEA.

R PROMORES: Peptidase S8; I.

R PROMITS; PROMORES: SUBTILASE ASP; I.

R PROSITE; PSOM136; SUBTILASE ASP; I.

R PROSITE; PSOM136; SUBTILASE ENS; I.

R PROSITE; PSOM139; SUBTILASE ENS; I.
                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.7%; Score 422.5; DB 17; Length Best Local Similarity 31.4%; Pred. No. 1.1e-16; Matches 138; Conservative 55; Mismatches 167; Indels
                                                                             Last sequence update)
Last annotation update)
                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQAYNVPSGPQRFSLAIV 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2003 (TrEMBLrel. 21, 01-JUN-2003 (TrEMBLrel. 24, Alkaline serine protease.
                                            PRELIMINARY;
                                                                                                                                                           NCBI_TaxID=2261;
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315 YIIGSPGAAEKAITVAAMAD----VGELGFN---LASFSSRGPTADGRIKPDIAAPGYNI 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 TAAK------ANSVNGYVTYSGTSMATPFVAGTVALMLN---ANPNLTPNDA--YN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 ALIAGATDVGLGYPSGDQGWGRVTLDKSLNVA------YVNEATALATGQKAT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 YSFQA-QAGKPLKISLVWTDAPGSTTASYTLVNDLDLVITAPNGGKYVGNDFSYPYDNNW 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSNLNTLFSQAWNAGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 VQNKDVYGIKVINLSLGTSTSSDG--TDSTSLAVNFAVD-----SGIVVVVAAGNSGPAK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 TIPYDDNGHGTHVASIAAGTGAGNSFYKGVAPDALLVGIKVLDANGSGSMSTVTAGIDWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRRBJ2;
QBTBJ2;
QBTBJ2;
QBTBJ2 (TFEMBLrel. 21, Created)
O1-UTN-2002 (TFEMBLrel. 21, Last sequence update)
O1-OCT-2003 (TFEMBLrel. 25, Last annotation update)
Subtlishin-like serine proteases.
APRE2 OR TTEOSA:
Thermoanserobacter tengcongensis.
Thermoanserobacteriaceae; Thermoanserobacteriales;
Thermoanserobacteriaceae; Thermoanserobacteriales;
WCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.8%; Score 402.5; DB 16; Length Best Local Similarity 31.0%; Pred. No. 1.3e-15; Matches 142; Conservative 63; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59968 MW; BA9C5C52F7083A18 CRC64;
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SEQUENCE 561 AA; 59968 M
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219 VEADLADSTAQIGAPRAWAGGNTGQGVEVAVLDTGVDAG-----HPDLADRIAARQSFV 272
                                                                     RTNNANDPNGHGTHVAGSVLGNAL----NKGMAPQANLVFQSIMDSSGGLGGLPSNLNT 112
                                                                                                                                                                                                         113 LFSQAWNAGARIHTNSWGA-PVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGFNSGTISA 171
                                                                                                                                                                                                                                                                          332 MEWAAVERHAKIVNMSLGSGEQSDGSDPMSRAVÖRLSAQTGALFVVAAGN-GGEAGSIGA 390
                                                                                                                                                                                                                                                                                                                                                                                        232 SLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAAL--- 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NSSFAAGGNGAYOSLSGTSMATPHVAGAAALL-----AAARPDLSGSALKDV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 IAGATDVGLGYPSGDQGWGRVTLDKSLNVAYVNEATALATGQK-----ATYSFQAQAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 KPLKISLVWTDAPGST---TASYTLV---NDLDLVIT-----APNGOKYVGNDFSYPYDN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545 VILELSVAATHAPEGVFRLSASRVTVPAHGTADVTLTIDGSGSAGGRAYSGQILA---T 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNANDPNGHGTHVAGSVLGN-ALN----KGMAPQANLVFQSIMDSSGGLGGLPS----- 108
                                                                                                             273 PDENTDDRDGHGTHVASTIAGTGAASAGKEKGVAPGARLSIGKVLDNS-GRGQISWTLAA
                                                                                                                                                                                                                                                                                                                                            PGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 LASSSHRIPRYDAFQAGSGRVDVDAAVRAGVYASAIAYAPGSSPGPVRRLVIYINIIGAA
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Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.5%; Score 377.5; DB 16; Length
Best Local Similarity 34.5%; Pred. No. 2.7e-14;
Matches 119; Conservative 48; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 AA; 45838 MW; 6D09A99BBC1E310F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 NWDGRNNVENVFINAPQSGTYTIEVQAYNVPSGPQRFSLAI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 30:3927-3935(2002).

BMBL, AP004601; BAC14331.1; -
60:0004289; F:subtilase activity; IEA.

GO; GO:0005508; P:subtilase and peptidolysis; IEA.

InterPro; IFR000209; Peptidase S8.

PRO0082; Peptidase S8.

PRINTS; PRO0023; SUBTILISIN.

PROSTIE; PS00136; SUBTILIASE ASP; 1.

PROSTIE; PS00136; SUBTILIASE HS; 1.

PROSTIE; PS00138; SUBTILASE HS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBENVI;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Intracellular alkaline serine proteinase.
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STRAIN=HTE831 / DSM 14371 / JCM 11309;
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SEQUENCE 430 AA
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Humben D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Nature 417:141-147(2002).
EMBL: AL999130: CACO1588.1; -.
HSSP; Q99405; 1MPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerdeno. A.W., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR003137; PA.
InterPro; IPR003197; PA.
   516 TGTQRQETITILPSQTGTYYVKVYSYR-GSGNYFFDLS 552
                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UND-2003 (TrEMBLrel. 24, Last annotation update)
Putative secreted peptidase.
SCO7188 OR SC8A11.16C.
                                                                                                                                                                           PRT; 1239 AA
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Pfam; PF0082; Peptidase S8; 1.
PRINTS; PR00723; SUBTILLSIN.
PROSITE; PS00136; SUBTILASE AIS; 1.
PROSITE; PS00138; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
                                                                                                                                                                                                                                             Created)
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MEDLINE=97000351; Pubmed=8843436;
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Best Local Similarity 30.6'
Matches 141; Conservative
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                                                                                                                                                                        PRELIMINARY;
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SEQUENCE 1239 AA
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Saunders D.C.
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Ogf PBZ4

ID QGF PBZ4

DT QGF PBZ4

DT QGF PBZ4

DT QGF PBZ4

OG GGF PBZ4

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                                                                                                                                       220 TAPGTFILSARS--SLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGI 277
                                                      231 WCIQNQSKYNINIL---SL&LGSDATEPAEGDPVVNAV------ETAWDNGMVVCVAA
                                                                                                                                                        -----NLNTLFSQAWNAGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDWTVLFAA
                                                                                        160 GNEGPNSGTISAPGTAKNAITVGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDV
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MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieeer H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowiteoff E., Rajandream M.A., Rutherford K., Rutter S.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                       T--PNQVKEKLMEACQD--LGQSPNVQGAGYL---NAANLININE 430
                                                                                                                                                                                       TPKPSLIKAALIAGATDVGLGYPSGDQGWGRVTLDKSLNVAYVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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GO:0004289; F:subtilase activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; Streptomyces.
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EMBL; AL939130; CAC01576.1; -.
HSSP; Q99405; IMPT.
                                                                                                                                                                                                                                                                                                                                          Putative secreted peptidase. SCO7176 OR SCBA11.04C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 G-APVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGATENYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 QSLSGTSMATPHVAGAAALLAAEH------PDWTGQRLKEALV-GTTAGTQRFSPF 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOGWGRVTLDKSLNVAYVNEATALATG-------OKATYSFQAQAGKPLK 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 GTGAASGGVEKGVAPGASLHIGKVLDNSG--SGQDSWV--LAGMEWAVRDQHAKIVSMSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 PSFGSLADNPNHIAQFSSRG-ATRDGRIKPDVTAPGTFILSARSSLAPDSSFWANYNSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 AYMGGISMATPIVAGNVAQL-REHFIKNRGITPKP----SLIKAALIAGATDVGLGYPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYGOGOVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAGSVL
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from
                                                                                                                                                                                                                                                                                                                                     15.8%; Score 357; DB 16; Length 1253;
.larity 30.0%; Pred. No. 1.7e-12;
Conservative 53; Mismatches 165; Indels 116
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Subtilishin-like protease.
Streptomyces albogriseolus.
Bacteria; Actinobacteria; Actinomycetales;
                                                                                                                                                                                                                                                                              1253 AA; 130971 MW; AA69B417EFEEDB89 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1887;
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J. Bacteriol. 179:430-438(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
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GO; GO:0008233; F:peptidase activity; IEA
                                   InterPro; IPR000209; Peptidase_S8.
Pfan; PP02225; PA; 1.
Pfan; PP02082; Peptidase_S8; 1.
PKINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_SER; 1.
Complete procteome.
SEQUENCE 1253 AA; 130971 MW; AA698
InterPro; IPR003137; PA.
InterPro; IPR000209; Peptidase_S8
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HSSP; P00782; 2SBT.
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                                                                                                                                                                                                                                                                  322 GMDTPETDPLEAA-----VDKLSAEKGILFAIAAGNEGPQS--IGSPGSADSALTVGA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 YNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITP--KPSLIKAALIAGATDVGLGYP 300
                                                                                                                                                                                                                                                                                                      GNALN-----KGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA--GARIHTNSWG 130
                                                                                                                                                                                                                                                                                                                         266 GTGAQSKGTYKGVAPGAKILNGKVLDDA----GFGDDSGILAGMEMAAAQGADIVNMSLG 321
                                                                                                                                                                                                                                                                                                                                                              131 A-----PVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAITVGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                      184 TENYRPSFGSLADNPHHIAQFSSRG-ATRDGRIKPDVTAPGTFILSARSSLAPDSSFWAN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                         422 KPAGYMTISGTSMATPHVAGAAALLKQQH-----PEWKYAELKGALTASTKDG--KYT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGDOGWGRVTLDKSLNVAYVNEATALATG------QKATYSFQAQAGKPLKIS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 PFEQGSGRVQVDKAITQTVIAEPVSLSFGVQQWPHADDKPVTKKLTYRNLGTEDVTLKLT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 LVWTDAPG-STTASYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAP 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATGPKGKAAPAGFFTLGASTLTVPA-NGTASVDVTADTRLGGAVDGTYSAYVVATGAG 591
                                                                                                                                                                                                                                              GLYGQGQVVAVADFGLDFGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAGSVL 77
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] - SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
A novel subtilisin-like serine protease from Thermoanaerobacter A novel subtilisin-like serine protease from Thermoanaerobacter yonseiensis KB-1: cloning, expression and biochemical properties."; Supmitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  75;
                                                                                                                                                                                      Length 1102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2] SEQUENCE FROM N.A.
Jang H.J., Kim B.C., Pyun Y.R., Kim Y.S.;
"Subtilisin-like protease, thermidin, from Thermoanaerobacter yonseii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoanaarobacter yonseii.
Bacteria, Pirmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
(VGBI_TaxID=111519;
                                                                                                                                                                                                                   Indels
                                                                                                                                                           F9E4AD2590FE559E CRC64;
GO; GO:0004289; F:subtilase activity, IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Thermicin (Subtilisin-like protease thermicin).
                                                                                                                                                                                      Query Match
15.4%; Score 347.5; DB 2;
Best Local Similarity 29.7%; Pred. No. 5.3e-12;
Matches 130; Conservative 52; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412
                        InterPro; IPR002860; GH BNR.
InterPro; IPR002860; GH BNR.
InterPro; IPR002039; Peptidase_S8.
Pfam; PR0012; PNR; 2.
Pfam; PR0012; PR011dase_S8. 1.
PRNYS; PR00123; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE ASP; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Procease; Serine procease.
SEQUENCE 1102 AA; 114128 MW; P9E4AI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 HVAGDAAGNGYASNGKYKGVAPEANIVAVKVLDSY----GRGSSSDILAGMQWVLDNKEK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 AGARIHTNSWG-APVNGAYTANSRQVDEYVR-----NNDMTVLFAAGNEGPNSGTISAP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 GTAKNAITVGATENYR-PSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 GTSRNAITVGAVDDKRTPDI-----EDDEVAKFSGRGGPY--LYKPDVVAPGVKIVSTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 SLAPDSSFWANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 NNYGLYGOGOVVAVADTGLDTGRNDSSMHEAF---RGKITALY-ALGRINNANDPNGHGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
          databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase, Protease, Serine protease.
SEQUENCE 412 AA, 44503 MW; E3C6A0F81B1A1D47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 345.5; DB 2; 35.5%; Pred. No. 1.9e-12; ive 39; Mismatches 113;
                                                                                                                                                      GO, GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; F:subtilase activity; IEA.
GO; GO:0006508; F:subtilase and peptidolysis;
InterPo; IPR00209; Peptidase_S8.
FRINTS; PR00723; SUBTILISIN.
PROSITE; PS00134; SUBTILISIN.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8 EMBL; AX028704; AXC27733.1; -. HSSP; Q45670; 1DB1.
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ATKINEAGL----WTQGSGMINIEEAL
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es 116; Conserv
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Protease. T. Yonsei Transglut Foreign p

Pyrococcu Hyperther

Protein e RP-III re Hyperther

Streptomy DhpA-mel

Fragment

Protease. Pyrococcu WO9856926

F. balust Streptomy

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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease A-1 from Bacillus sp NCIB12289 described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN
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Aaw94841
Abw94841
Abb09483
Abb09483
Aaw1366
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Aaw841008
Aaw94839
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100.0%; Pred. No. 1.3e-160;
iive 0; Mismatches 0;
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AAW94841
AAW24123
ABB09483
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ABU07391
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AAW13668
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AAR27481
AAR87007
AAR87008
AAW24124
AAW94839
AAY08471
ABP76735
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12-APR-2001; 2001JP-00114048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 434; Conservative
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 Hatada Y, Ogawa A,
Okuda M, Saeki K;
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 (KAOS ) KAO CORP
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                                                                                                                                                                                                                           434
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                                                                                                                                                                                      US-09-985-689A-6
2250
1 NDVARGIVKADVAQSSYGLY.......EVQAYNVPQGPQAFSLAIVN
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                  version 5.1.6
- 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                    protein search, using sw model
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Nomura·M;
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Best Local Similarity
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              Sequence 434 AA;
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12-APR-2001; 2001JP-00114048
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Saeki K;
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protease, Bacillus, casein digestion, oleic acid, enzyme, composition, oxidising agent.
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AAY17090 standard; protein; 640
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                                                                                                                  Bacillus alkaline protease.
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                                              The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg: C it is stable over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the enzyme to be an effective component of washing compositions including bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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95.2%; Score 2143; DB 2;
Best Local Similarity 93.5%; Pred. No. 2.5e-152;
Matches 406; Conservative 19; Mismatches 9;
                 Disclosure; Page 58-63; 71pp; Japanese.
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21-JUL-1999
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The invention relates to alkaline proceases produced by strains of Bacillus. The proceases ability to digest casein is not inhibited by cleid acid and they have a high stability to exidising agents. The cleid acid and they have a high stability to exidising agents. The is active over the pH range 4-13 and has at least 80% of its optimum active over the pH range 4-13, (b) after 30 minutes at 40 deg. C it is cable over the pH range 6-11; (b) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-FAGE. The alkaline proceases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to exidising agents allows the beaches. The present sequence represents an alkaline procease. (Updated to 20-MAR-2003 to correct DR field.)
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                                                                                                                                    Kageyama
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                                                                                                                                                                                                                   Alkali protease from Bacillus used in washing powders
                                                                                                                                   Hitomi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.2%; Score 2141; DB 2; 93.5%; Pred. No. 3.6e-152; iive 19; Mismatches 9;
                                                                                                                                   Kubota H,
                                                                                                                                                                                                                                             Disclosure, Page 63-68; 71pp; Japanese.
                                                                                                                                   Saeki K,
                                                    98WO-JP004528
                                                                              97JP-00274570
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Best Local Similarity 93.5
Matches 406; Conservative
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                                                                                                                                                                         WPI; 1999-287736/27.
N-PSDB; AAX37279.
                                                                                                                                   Okuda M,
Nomura M
                                                                                                         (KAOS ) KAO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 640 AA;
                                                    07-OCT-1998;
                                                                                07-OCT-1997;
                          15-APR-1999
                                                                                                                                   rakaiwa M,
Shikata S,
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Disclosure; Page 53-58; 71pp; Japanese.
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                                          434
                                                                  VPVGPONFSLAIVN 434
                                                                                                                                                                                                                                Bacillus alkaline protease
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(first entry)
                                          VPQGPQAFSLAIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okuda M,
Nomura M;
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21-JUL-1999
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Matches 400;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel Bacillus sp. alkaline proteases useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease KP9866 from Bacillus sp strain XSM-KP9860 described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NDVARGIVKADVAQSSYGLYGGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                                                                                                                                                                                                                                                        Sumitomo N;
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                                                                                                                                                Alkaline protease; detergent; laundry; bleaching; dishwasher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.7%; Score 2130; DB 5; Length 434; 92.4%; Pred. No. 1.4e-151; ive 24; Mismatches 9; Indels (
                                                                                                                        Bacillus sp KSM-KP9860 alkaline protease protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                           detergent
                                                                                                                                                                                                                                                                                                                                                        Araki H,
                                                                                                                                                                                                                                                                                                                                                                                                                          New modified alkaline proteases useful in
                                                                                                                                                                                                                                                                                                                                                        Sato T,
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                                                                                                                                                                                                                                                                                                                                                        Kageyama Y,
                                          AAM50081 standard; protein; 434
                                                                                                                                                                                                                                                                                    22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
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Saeki K,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-437518/47.
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The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by cleid acid and they have a high stability to exidising agents. The cleid acid and they have a high stability to exidising agents. The is active over the prange 4-13 and has at least 80% of its optimum active over the pH range 4-13 and has at least 80% of its optimum at a table over the pH range 6-11; (b) after 30 minutes at 40 deg. Cit is cable over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43.000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to exidising agents allows the beaches. The present sequence repairs of washing compositions including bleaches. The present sequence results an alkaline proteases. (Updated on 20-MAR-2003 to correct DR field.)
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Alkaline protease, Bacillus, casein digestion; oleic acid; enzyme; washing composition; oxidising agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%; Score 2122; DB 2;
ilarity 92.2%; Pred. No. 9.5e-151;
Conservative 24; Mismatches 10;
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Sloma A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38$) compared to prior art alkaline proteases (31 and 23$). This sequence represents a fragment of the alkaline protease A-2 from Bacillus sp NCIB12513 described in the method of the invention
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                                                                                                                                                                506 PNGNQGWGRVTLDXSLNVAYVNESSALSTSQKATYTFTATAGKPLKISLVWSDAPASTTA
                                                                                                                                                                                                                 566 SVILVNDLDLVITAPNGTRYVGNDFSAPFDNWMDGRNNVENVFINSPQSGTYTIEVQAYN
AGARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
              AGARIHTINSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNERPNGGTISAPGTAKNAI
                                                TVGATENLR PSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                       386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                  WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                446 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGY
                                                                                                                                                   PSGNOGWGRVTLDKSLNVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified alkaline proteases useful in detergent compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.1%; Score 2116.5; DB 5; Length 433; larity 92.2%; Pred. No. 1.4e-150; Conservative 21; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sumitomo
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alkaline protease; detergent; laundry; bleaching; dishwasher.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus sp alkaline protease protein A-2 fragment.
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                                                                                                                                                                                                                                                                                                                                           AAM50086 standard; protein; 433 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kageyama Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
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                                                                                                                                                                                                                                                      VPOGPOAFSLAIVN 434
                                                                                                                                                                                                                                                                             VPVGPONFSLAIVN 639
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Best Local Similarity
Matches 400; Conservat
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Okuda M, Saeki K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 433 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus sp.
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361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
ndvargivkadvaonnfglygogojvavadtgldtgrndssmheafrgkitalyalgrtn
                                      NANDPNGHCTHVAGSVLGNAT-NKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                                              WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                                                            PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA
                      NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS
                                                                     AGARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                   TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                 Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease; detergent; surfactant; leather processing; debittering;
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/note= "mature protein"
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.e= "prepro region"
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                                                                                                                                                                                                                                                                                                                                                                                             AAW89547 standard, protein;
                                                                                                                                                                                                                                                                                                           VPQGPQAFSLAIVN 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus JP170 protease.
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N-PSDB; AAV82382.
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Location/Qualifiers

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                    This is the amino acid sequence of a novel protease of Bacillus sp. JP170 (NCIB 12513), as deduced from the nucleotide sequence of an isolated gene (see BAN82392). The entire protein, including the signal peptide and prepror region, has 77% identity to alkaline protease Y (see AAM89548) from Bacillus. The invention provides vectors, recombinant host cells and methods for the recombinant production of the protease The protease is used in laundry and dishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the degree of hydrolysis of protein hydrolysates, for flavour degree of hydrolysis of protein characters, for flavour development through hydrolysis of proteins can be considered stability towards oxidation under alkaline conditions, it has enhanced stability towards oxidation under alkaline conditions, to towards bleaching agents of the protease activity is diminished. Such provides mutant cells in which the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
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                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protease, Bacillus, casein digestion, oleic acid; enzyme,
composition, oxidising agent.
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                                                                                                                                                                                                                                                     94.1%; Score 2116.5; DB 2; Length 641; 92.2%; Pred. No. 2.5e-150; ive 21; Mismatches 12; Indels 1;
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Claim 7; Page 53-54; 77pp; English.
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Best Local Similarity
Matches 400; Conserv
                                                                                                                                                                                                                               Sequence 641 AA;
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21-JUL-1999
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washing c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to alkaline proceases produced by strains of Bacillus. The proceases ability to digest casein is not inhibited by obleic acid and they have a high stability to oxidising agents. The alkaline procease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proceases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the enzyme to be an effective component of washing compositions including bleaches. The present sequence represents an alkaline protease of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSGNOGWGRVTLDKSLNVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVTLVNDLDLVITAPNGTKXVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bleaches. The present sequence represents an alkaline protease of invention. (Updated on 20-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                                                                                                                                                                                                         Kubota H, Hitomi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alkali protease from Bacillus used in washing powders
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91.5%; Pred. No. 9.6e-148;
cive 14; Mismatches 23;

    639
/note= "all residues indicated
acids"

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                                                                                                                                                                                                                        98WO-JP004528
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Best Local Similarity 91.5%
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Okuda M,
Nomura M;
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                                                                                                                                                                                                                                                                                                                                      CORP.
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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38$) compared to prior art alkaline proteases (31 and 23$). This sequence represents a fragment of the alkaline protease SD-521 from Bacillus sp strain SD-521 (FERM BP-11162) described in the method of the
447 WANHDSKYAYMGGTSMATPIVAGNVAQIREHFVKORGITFKPSLLKAALIAGAADKGGY
                                                                                                                                                                                                                                                          PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                                                                                                                                                                                                                              SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVBVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp SD-521 (FERM BP-11162) alkaline protease protein fragment.
                                                   AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                         AGARIHTINSWGAAVNGAYTIDSRNVDDYVRKNDWILLFAAGNEXPNGGTISAPGTAKNAI
                                                                                                                      TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                                                                                       387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTXILSARSSLAPDSSF
                                                                                                                                                                                        WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified alkaline proteases useful in detergent compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alkaline protease; detergent; laundry; bleaching; dishwasher.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2024.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM50084 standard; protein; 433
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12-APR-2001; 2001JP-00114048.
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Okuda M, Saeki K;
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                    267
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    .640
/note= "all residues indicated as Xaa are arbitrary amino
acids"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                       protease, Bacillus, casein digestion; oleic acid; enzyme;
composition; oxidising agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alkali protease from Bacillus used in washing powders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hitomi J,
                                                                                                                                                                                                                                                          An alkaline protease sequence from Bacillus species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 50-53; 71pp; Japanese.
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                                                                                                                                   AAY17088 standard; protein;
                    434
                                                 VPVGPOXFSLAIVN 639
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Matches 397, Conservative
                    VPQGPQAFSLAIVN
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Nomura M;
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1998;
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21-JUL-1999
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                                                                NANDPNGHCTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120
                                                                                                                                                                                                                               proteases useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency
                                                                            WANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY
                                                                                                                                                                                                                                                         SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                             1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN
                                            NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                       AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                           TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                                                                                        WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
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            Gaps
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           Indels
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 Pred. No. 1.2e-143;
8; Mismatches 21;
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ilarity 88.5%; Pre
Conservative 28;
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12-APR-2001; 2001JP-00114048.
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Saeki K;
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  Best Local Similarity
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           Matches
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(34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease E-1 from Bacillus sp strain D6-(FBRM-P1592) described in the method of the invention
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                                                                                                                                                                                                                                                                          SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNMDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                   360 SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNWDGRNNVENVFINAFQSGTYTIEVQAXN
                                                                                                                                                                               TVGATENIRPSFGSYADNINHVAQFSSRGPTKDGKIKPDVMAPGTFILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                          WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                                                                                                                                                                                                        PSGNOGWGRVTLDKSLNVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                                                                                                                                                                                                                                                                                                                       AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                                                                                                             NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS
                                                                                             Gaps
                                                                                                                     1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alkaline protease Y; detergent; surfactant; leather processing; debittering; flavour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease from Bacillus subtilis LC20 - useful in laundry
                                                                                             7;
                                                                      Length 433;
                                                                                             Indels
                                                                      Query Match 89.8%; Score 2020.5; DB 5;
Best Local Similarity 88.2%; Pred. No. 2.3e-143;
Matches 383; Conservative 28; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp. alkaline protease Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW89548 standard;
                                                  Seguence 433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9856927-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW89548;
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This is the amino acid sequence of a Bacillus sp. alkaline protease Y detergency. It shows 77% identity to a newly isolated protease and improved detergency. It shows 77% identity to a newly isolated protease (see AAW89547) of Bacillus sp. UPIV (NCIB 12513). The invention provides vectors, recombinant host cells and methods for the recombinant production of such proteases. The protease are used in laundry and dishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the degree of hydrolysis of protein hydrolysates, for flavour development through hydrolysis of proteins, degradation of undesized peptides and in enzymatic synthesis of peptides. They have enhanced stability towards peroxy type. The invention also provides mutant cells in which the protease activity is diminished. Such cells can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.6%; Score 2016.5; DB 2; Length 636; 88.0%; Pred. No. 8e-143; ive 30; Mismatches 21; Indels 1;
            for leather processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production of heterologous recombinant proteins
                                                                                                                                                                                                                                Page 55-56; 77pp; English
                        dishwashing detergents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.0
Matches 382; Conservative
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\mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times \mathbb{F}_{\mathbf{X}} \times 
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۲; 240 300 502 360 562 420 120 180 442 264 NASDPNGHGTHVAGSVLGNAL-NKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN 322 382 1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN 60 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 383 TVGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF SYTLVNDLDLVITAPNGCKYVGNDFSAPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYN NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN Gaps ۲; VPSGPQRFSLAIVH 636 VPOGPOAFSLAIVN 434 443 361 503 181 241 301 421 623 61 121 g ద D D g à dd g g \$ ò 8 à ò δ

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1;

2; Length

Query Match
Best Local Similarity 87.8%; Pred. No. 1.3e-142;
Matches 381; Conservative 30; Mismatches 22; Indels

Sequence 433 AA;

9 09 120

180 179 240 239 300 299 360 359 420 419

PSGDOGMGRVTLDKSLNVAYVNEATALATGOKATYSFQAQAGKPLKISLVWTDAPGSTTA

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SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 360 SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNWDGRNNVENVFINAPQSGTYIIEVQAYN

VPQGPQAFSLAIVN 434

421

TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY PSGNOGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA

AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI

121 120 181 180 241 240 301 300 361

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61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS

1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN

The sequence is that of alkali-protease Ya enzyme which can be used in the recombinant production of Ya enzyme. Ya enzyme is excellent in alkali resistance and surface active agent resistance and improves detergency

DNA coding alkali-protease Ya enzyme - has good alkali and surfactant resistance and improves detergency.

WPI; 1992-288440/35 N-PSDB; AAQ27516.

(LIOY) LION

90JP-00327110 90JP-00327110

28-NOV-1990; 28-NOV-1990;

JP04197182-A.

16-JUL-1992

Claim 2; Page 1; 17pp; Japanese.

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Bacillus lion Y protease; polyethylene glycol; PEG; soap; methoxypolethyleneglycol; mPEG; skin; hair care product; cosmetic;
                                                                                                                                                       Modified Bacillus lion Y protease.
                                                                        AAW61495 standard, protein; 433
         433
                                                                                                                                (first entry)
|| || || || || || || || vpsgporfslaiuh
                                                                                                                                06-NOV-1998
           420
                                                                                                      AAW61495
                                                surface active agent resistance; detergency improver.
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433

enzyme

Alkali-protease Ya Alkali resistance;

05-FEB-1993

AAR26274

sp.

Bacillus

AAR26274 standard; protein;

RESULT 14 AAR26274

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New enzyme modified by attachment of many polymeric molecules - useful in skin and hair care products, has reduced tendency to cause sensitisation and increased stability.
                                                    /note= "The enzyme is modified by methoxypolethyleneglycol molecules covalently attached to the N-terminal amino group and to fourteen unspecified amino groups of lysine residues present on the surface of the enzyme"
lipstick; hair gel; sun oil; shampoo; hair dye; insect repellant.
                                                                                                                                                                                                                                                                          Claim 16; Page 44-45; 56pp; English.
                                    Location/Qualifiers
                                                                                                                                                       97DK-000000038.
                                                                                                                                      98WO-DK000015
                                                                                                                                                                                  (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                     WPI; 1998-399132/34.
                                    Key
Modified-site
                                                                                                                                                      10-JAN-1997;
25-JUN-1997;
                                                                                                  WO9830682-A1
                                                                                                                                     12-JAN-1998;
                 Bacillus sp
                                                                                                                   16-JUL-1998
                                                                                                                                                                                                   Olsen AA,
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The present sequence represents the Bacillus lion Y protease. The invention claims for enzymes covalently modified on their surface by the attachment of a large number of small polymentic molecules, e.g. tatachment of a large number of small polymentic molecules, e.g. polyethylene glycols (PEG). The polymeric molecules are coupled to the N-terminal amino group and the amino groups of lysine residues found on the surface of the enzyme. In the example given, the lion Y protease was modified using methoxypolethyleneglycol (mPEG) as the polymeric molecule. The N-terminal amino group and the amino groups of the fourteen lysine residues present on the surface of the lion Y protease were modified. Modification of the enzymes increases the stability and/or reduces the sensitising potential (allergenicity) of the enzyme, without sensitising potential (allergenicity) of the enzyme, without relatively reducing enzymatic activity. Also, using a large number of relatively small polymeric molecules, rather than a few very large ones, provides a more even effect with reduced activity loss. The modified and hair care products, e.g. soaps, cosmetics, creams, gels, libsticks, hair gels, sun oils, shampoos, hair dyes, insect repellants, etc.
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Best Local Similarity
Matches 381; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 433 AA;
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241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300

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DD 240 WANYNSKYAYMGGTSNATPITAGNVAQLREHPIKNRGITPKPELIKAALIAGATDVGLGY 299

QY 301 PSGNQGWGRVTLDKSINVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWEDAPASTSA 360

DD 300 PSGDQGWGRVTLDKSINVAYNBATALATGGGATYSFQAQAGKPLKISLVWTDAPSGSTTA 359

QY 361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTTUFVQAYN 410

DD 360 SYTLVNDLDLVITAPNGCKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYN 419

QY 421 VPQGPQAFSLAIVN 434

DD 420 VPSGPQRFSILAIVH 433

Search completed: March 31, 2004, 16:04:333
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US-09-96-921A-2
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  361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 NDVARGIVKADVAQSSYGLYGQQQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDWTILFAAGNERPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TVGATENLRPSFGSYADNINHVAQFSSRCPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 WANHDSKYAYMGGTSMATFIVAGNVAQLREHFVKORGITPKPSLLKAALIAGAADVGLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVTLVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS
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                                                                                                                                                                                                 US-UY-509-814A-4

Sequence 4, Application US/0950814A

PATELICANT: TAKATRA, MIKIO
APPLICANT: TAKATRA, MIKIO
APPLICANT: TAKATRA, MIKIO
APPLICANT: WIBOTA, HIROMIA
APPLICANT: WIBOTA, HIROMIA
APPLICANT: WIBOTA, HIROMIA
APPLICANT: WIBOTA, HIROMIA
APPLICANT: WIBOTA, HIROMIA
APPLICANT: WIBOTA, WASAFUH
APPLICANT: WONDAA, US/09/509,814A
CURRENT APPLICATION WIBER: PCT/JP98/04528
FRIOR APLICATION NUMBER: PCT/JP98/04528
FRIOR FILING DATE: 1999-106-07
FRIOR FILING DATE: 1999-106-08
NUMBER: OF SEQ ID NOS: 24
SEQ ID NO 4
LENGTH: 639
LENGTH: 639
LENGTH: 639
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                                                                                 VPOGPOAFSLAIVN 434
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Best Local Similarity 92.2%;
Matches 400; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-4
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                                                                                                                                         SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                               567 SVILVNDLDLVITAPNGTQYVGNDFTSPYNDNMDGRNNVENVFINAPOSGTYTIEVQAYN 626
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                                                              PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA
                                                                                   507 PNGNQGMGRVTLDKSLNVAXVNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA
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Gaps
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95.2%; Score 2141; DB 4; Length 640;
Best Local Similarity 93.5%; Pred. No. 3.9e-165;
Matches 406; Conservative 19; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: TAKAIWA, MITSUYOSHI
APPLICANT: SAEKI, KARISUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SOURCE, 0327-0632-0507
TILE REFERENCE: 0327-0632-0507
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT APPLICATION NUMBER: US/09/509,814A
PRIOR APPLICATION NUMBER: US/09/509,814A
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALCATION VESION 3.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09509814A Patent No. 6376227
                                                                                                                                                                                                                                                         627 VPVGPQTFSLAIVN 640
                                                                                                                                                                                                                           VPOGPOAFSLAIVN 434
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                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-09-509-814A-8
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568 SITLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 627
361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: TAKANA, MIKIO
APPLICANT: SARZI, KATSUHISA
APPLICANT: SARZI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
TITLE REFRENCE: 0327-0823-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT APPLICATION NUMBER: US/099804528
FRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
CURRENT FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
LENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACATURE SECTIONS SP.
FERATURE

NAME/KEY: misc feature
LOCATION: (23)...(23)

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (29)...(29)

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (32)...(32)

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (45)...(46)

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)...(47)

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)...(47)

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)...(47)

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (53)...(53).
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LOCATION: (74)...(74)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (89)...(89)
OTHER INFORMATION: Xaa is any amino acid
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NAME/KEY: misc feature
LOCATION: (128)..(129)
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INFORMATION: Xaa is any amino acid
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INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09509814A, Patent No. 6376227, GENERAL INFORMATION:
                                                                                                                    421 VPQGPQAFSLAIVN 434
                                                                                                                                                       NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Bacillus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI 180
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                                                                        Sequence 42, Application US/08873479
Fatent No. 5891701
GENERAL INFORMATION:
APPLICANT: NORMATION:
APPLICANT: Lynne, Christianson
ITILE OF INVENTION: Nucleic Acids Encoding A Polypeptide
ITILE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58917010 No. 5891701disk of No. 5891701th America STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
CONNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.1%; Score 2116.5; DB 2; Length 641; Best Local Similarity 92.2%; Pred. No. 3.8e-163; Matches 400; Conservative 21; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DESCRIPE
COMPUTER: FASTENCE
SOFTWARE: FASTENCE
SOFTWARE: FASTENCATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: AGFIS: Cheryl H
RECTSTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELESPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS: LENGTH: 641 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
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INFORMATION: X	/KEY: misc featur FION: (130)(130 R INFORMATION: Xa. /KEY: misc featur	CATION: (131)(131 HER INFORMATION: Xa. ME/KEY: misc featur	rion: (132)(132 r INFORMATION: Xa KEY: misc featur	ION: (133) (133 INFORMATION: Xa	/KEY: misc_featu FION: (146)(14 R INFORMATION: X	/KEY: misc featur FION: (148)(148	AME/KEY: misc featur ACMIN: (160)(160	CEY: misc featur ION: (165)(165	INFORMATION: Xa CEY: misc featur	(172)(172)RMATION: Xa	(183). (183)RMATION: Xa	misc featur (187)(187 RMATION: Xa	misc_featur (188)(188 XRMATION: Xa	misc featur (189)(189	MMATION: Xa misc featur	(194)(194 RMATION: Xa	misc featu (286)(28 DRMATION: X	CEY: misc featur ION: (306)(306 INFORMATION: Xa	XEY: misc featur ION: (324)(324	INFORMATION: Xa KEY: misc featur TON: (369) (369	INFORMATION: Xa KEY: misc featur	ION: (431)(4	feat 7(5	EY: misc featur ON: (531)(531	INFORMATION: Xa	ION: (541)(541 INFORMATION: Xa	OCATION: (584)(584) THER INFORMATION: Xa	NAME/KEY: misc feature LOCATION: (591)(591) OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NANDPNGHGTHVAGSVLGNGTSNKGWAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 NANDTWGHGTHVAGSVLGNGXTNKGWAPQANLVFQSIMDSXGGLGGLPSNLQTLFSQAXS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI 180
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92.5%; Score 2082; DB 4; Length 6
Best Local Similarity 91.5%; Pred. No. 2.4e-160;
Matches 397; Conservative 14; Mismatches 23; Indels
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Retent No. 6376227

GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIXIO
APPLICANT: OKUDA, MITSOTOSHI
APPLICANT: WASEKI, KATSUHISA
APPLICANT: WIGOTA, HIRONI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SHITSUW
APPLICANT: SHIKATA, SHIKATA, SHIKATA, SHIRATA, NAME/KEY: misc_feature
LOCATION: (592)
JOHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (594)
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US-09-509-814A-2
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CURRENT FILING DATE: 2000 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-10 PRIOR FILING DATE: 1997-06 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin version EQ ID NO 2 LENGTH: 640 TYPE: PRT	misc_fea (3)(3) NRMATION: misc_fea	. (24) ION: Xaa i feature . (30)	AMATT (33). (33). AMATT	RMATION: misc fea (48)(4	MATION: nisc_fea (54)(5	Nisc fe	INFORMATION EY: misc_fe ON: (75) (misc fea	INFORMATION: XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	INFORMATION: Xaa KEY: misc feature ION: (106)(106)	DRMATION: X misc featu (129)(12 DRMATION: X	XEY: misc feature ION: (131)(131) INFORMATION: Xaa i XEY: misc feature	TION: (132)(R INFORMATION: /KEY: misc fea	HER INFORMATION: Xaa i ME/KEY: misc feature CATION: (134)(134)	KEY: misc feature ION: (147)(147) INFORMATION: Xaa KEY: misc feature	TION: (149)(149 R INFORMATION: Xa /KEY: misc featur	(161)(161 ORMATION: Xa misc_featur
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LOCATION: (166)(166) OTHER INFORMATION: Xaa NAMEKEY: misc feature LOCATION: (173)(173) OTHER INFORMATION: Xaa NAMEKEY: misc feature 1.00ATTON: (184)	, m) .	. 00 0) · × 0	7 do . z	0 . 2		. 20	z 0 · 2	. 0 - 2	(a) · Z	6) · Z	0 · Z	0 . 2	3 - X 0	- E 8	- z 9	- z ö	·ż	Query Match Best Local Similarity 9 Matches 397; Conservati

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TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
STRAIN: Bacillus sp.
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US-09-019-532-4
            ; TOPOLOGY:
; MOLECULE TYPE;
; ORIGINAL SOUR
; STRAIN: BU
US-09-104-623A-4
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CITY: NAW YORK
STREET: 405 Lexington Avenue
CITY: NAW YORK
STREET: BNC COUNTRY: USA
ZIP: 10174 LEXINGTON Avenue
COUNTRY: USA
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                                                                207 NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 266
                                                                                                                                                                                                                                                                                           327 AGARIHTNSWGAAVNGAYTIDSRNVDDYVRKNDMILFAAGNEXPNGGTISAPGTAKNAI 386
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                           NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN
                                                                                                                                          NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS
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APPLICANT: Patum, Tine Muxoll
APPLICANT: Deussen, Heinz-Josef
APPLICANT: Roggen, Erwin Ludo
TITLE OF INVENTION: A Modified Polypeptide
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63037520 No. 6303752disk c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-104-623A-4
; Sequence 4, Application US/09104623A
; Patent No. 6303752
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amino acid
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Length 433;
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                                                                 Indels
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APPLICANT: Olsen, Arne Agerlin
APPLICANT: Prent , Annette
TITLE OF INVENTION: A Modified Enzyme for Skin Care
FILE REPERENCE: 4922.204-US
CURRENT APPLICATION UNMER: US/09/019,532B
CURRENT FILING DATE: 1998-02-05
BARLIER APPLICATION NUMBER: 0038/97
BARLIER APPLICATION NUMBER: 0074/97
BARLIER APPLICATION NUMBER: 60/051,381
BARLIER APPLICATION NUMBER: 60/051,381
BARLIER PILING DATE: 1997-07-07
BARLIER FILING DATE: 1997-07-07
BARLIER FILING DATE: 1998-01-12
SARLIER FILING DATE: 1998-01-12
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89.4%; Score 2010.5; DB 4;
Best Local Similarity 87.8%; Pred. No. 8.4e-155;
Matches 381; Conservative 30; Mismatches 22;
                                                                     22;
Query Match

89.4%; Score 2010.5; DB 4.

Best Local Similarity 87.8%; Pred. No. 8.4e-155;

Matches 381; Conservative 30; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09019532B Patent No. 6416756; GENERAL INFORMATION:
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PSGDQGWGRVTLDKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTA 359
                                                                                                                                                                                                                                                                            361 SVILVNDLDLVITAPNGIKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                                                                                                                                                                        SYTLYNDLDLVITAPNGQKYVGNDFSYPYDNWDGRNNVENVFINAPQSGTYIIEVQAYN 419
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20 AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI 179
                                        TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                             241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
                                                                                                                                             240 WANYNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY
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APPLICANT: Slow, Alan
APPLICANT: Slow, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
CORRESPONDESS: No. 5891701 No. 5891701disk of No. 5891701th America
STREET: 405 Lexington Avenue
CITY: Now York
STATE: NY
COUNTRY: USA
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llarity 87.8%; Pred. No. 1.4e-154;
Conservative 30; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPARE: IBM Compatible
OMPARE: FastSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/873,479
FILING DATE: 12-UN 1997
CLASSIFICATION: 530
ATTORNEY AGENT INPORMATION:
NAMB: AGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5251.000-US
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US-08-873-479-43
Sequence 43, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Simi
Matches 381;
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US-08-873-479-43
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87.8%; Pred. No. 8.4e-155;
ive 30; Mismatches 22; Indels
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Patent No. 663826
GENERAL INFORMATION
APPLICANT: Deussen, Heinz-Josef
APPLICANT: Deussen, Heinz-Josef
APPLICANT: Other, Arne A.
APPLICANT: Fatum, Tine M.
APPLICANT: Roggen, Erwin L.
APPLICANT: Roggen, Erwin L.
APPLICANT: Roggen, Erwin L.
CURRENT REPERSINES: 5619.200-US
CURRENT PILION DATE: 1999-06-23
EARLIER APPLICATION NUMBER: PA.1998 00809
EARLIER APPLICATION NUMBER: PA.1998 00809
EARLIER APPLICATION NUMBER: 60/091,461
EARLIER PILING DATE: 1998-06-23
SERLIER PILING DATE: 1998-06-23
SOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 6
LENGTH: 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 VPQGPQAFSLAIVN 434
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Best Local Similarity 87.84
Matches 381; Conservative
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US-09-338-746-4
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US-09-338-746-4
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241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300
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US-09-196-281-13
Sequence 13, Application US/09196281A
Sequence 13, Application US/09196281A
Sequence 13, Application US/09196281A
Sequence 13, Application US/09196281A
Therman Mikelsen, Peter K.
APPLICANT: BANGIZ, Peter K.
APPLICANT: Mikelsen, Frank
TILLE OF INVENTION: Protease Variants And Compositions
FILE REPRENCY: 5435.200-US
CURRENT APPLICATION NUMBER: US/09/196,281A
CURRENT APLICATION NUMBER: 132/97
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                         Sequence 10, Application US/09515150A
Patent No. 655838
GENERAL INFORMATION:
APPLICANT: Handitz, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Handitz, Peter
APPLICANT: Handitz, Peter
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Proteuse Variants and Compositions
FILE REPRENCE: 5348.204.04
CURRENT APPLICANION NUMBER: US/09/515,150A
CURRENT APPLICANION NUMBER: US/09/515,150A
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Version 3.1
SEQ ID NO 10
                                                                PNGNGGWGRVTLDKSLNV 345
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CRGANISM: Bacillus
US-09-515-150A-10
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                           TVGATENYRPSFGSIADNPWHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF
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NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVPQSVMDSNGGLGGLPSNVSTLFSQAYS
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69.4%; Score 1562.5; DB 4; Length 345;
Best Local Similarity 92.5%; Pred. No. 1.1e-118;
Matches 294; Conservative 16; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASPULLATION OF STATE OF SECURITY HARDEN, PETER APPLICANT: Hansen, Peter APPLICANT: MAKALSEN, Frank APPLICANT: ANGERSEN, Rim TITLE OF INVENTION: Procease Variants and Compositions FILE REFERENCE: 5349,204-US CURRENT FILING DATE: 2000-02-24 NUMBER OF SEQ ID NOS: 12 SOFTWARE PATENTIN VERSION 3.1 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPSGPORFSLAIVH 635
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ORGANISM: Bacillus
US-09-512-251A-10
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365 TPINDYYTKASGISWATPHVSGVGALILQ---AHPSWTPDKVKTALIETADIVAPKEIAD 421
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J. APPLICANT: TAKAKURA, HIKATU
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
J. APPLICANT: HIMOOO, Tomoko
APPLICANT: ASADA, KIVOZO
APPLICANT: KATO, Ikunoshin
J. TITLE OF INVERTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT APPLICATION NUMBER: 1999-12-06
PRIOR APPLICATION NUMBER: 1999-12-06
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 12
ENGTH: 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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              TAKAKURA=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 EVQAYNVPQGPQAFSLAIVN 434
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REFERENCE/DOCKET NUMBER: TAK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR EDG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: peptide
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US-08-894-818B-1
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Sequence 1, Application US/08894818B

Patent No. 6261822

GENERAL INFORMATION:
APPLICANT:
APPLICANT: MORISHITA, Mio
APPLICANT: YAMMOTO, Katsuhiko
APPLICANT: YAMMOTO, Katsuhiko
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: TSUNASAMA, Susumu
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
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APPLICANTICA
                                                                                                                                                                       Query Match 69.4%; Score 1562.5; DB 4; Length Best Local Similarity 92.5%; Pred. No. 1.1e-118; Matches 294; Conservative 16; Mismatches 7; Indels
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTONENYAGENT INFORMATION:
NAME: BCCACL.
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: United States of America
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REGISTRATION NUMBER:
LENGTH: 345
TYPE: PRT
ORGANISM: Bacillus
                                                                            , UKGANALL...
US-09-196-281-13
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                                                                                         67 GHGTHVAGSVLGNGTSNK---GMAPQANLVFQSVM--DSNGGLGGLPSNVSTLFSQAYSA 121
                                                                                                                                                         242 ANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITP---KPSLLKAALIAGATDIG- 297
                                                                                                                                                                                                                                                                                                                                                                 365 TPINDYYTKASGTSMATPHVSGVGALILQ---AHPSWTPDKVKTALIETADIVAPKEIAD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 PASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTV 414
                                                                                                                                                                                                         122 GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAIT 181
                                                                                                                                                                                                                                                                           182 VGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFW 241
                                                                                                                                                                                                                                                                                                                                                                                                                298 LGYPSGNQGWGRVTLDKSL---NVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDA 354
                                                                   8 VKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHBAFRGKITAIY-ALGRTNNANDFN 66
                                  63; Gaps
Query Match 20.0%; Score 450.5; DB 4; Length 659; Best Local Similarity 31.4%; Pred. No. 3.1e-28; Matches 138; Conservative 69; Mismatches 170; Indels 63;
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Search completed: March 31, 2004, 16:11:56 Job time : 15.0215 secs

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March 31, 2004, 16:09:09; Search time 33.2177 Seconds (without alignments) 3418.697 Million cell updates/sec
                                                                                                                   US-09-985-689A-6
2250
1 NDVARGIVKADVAQSSYGLY.........EVQAYNVPQGPQAFSLAIVN 434
                                                                                                                                                                                                                                                                                                                                 1065169
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        1065169 segs, 261661801 residues
                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                                                                                   Scoring table:
                                                OM protein
                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                             Database
                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 6, Appli	Seguence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 13, Appl	Sequence 12, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 16, Appl	Sequence 13251, A
SUMMARIES	аг	US-09-985-689A-6	US-09-985-689A-1	US-10-385-662-2	US-09-985-689A-2	US-09-985-689A-7	US-09-985-689A-5	US-09-985-689A-3	US-09-985-689A-4	US-10-336-324-10	US-10-403-105-13	US-10-090-624-12	US-10-090-624-1	US-10-090-624-4	US-10-090-624-16	US-10-156-761-13251
		10	10	15	10	10	10	10	10	14	14	13	13	13	13	14
	Query Match Length DB	434	434	434	434	433	433	433	433	345	345	629	412	522	654	1208
de	Query	100.0	95.2	95.2	94.7	94.1	90.0	89.8	89.1	69.4	69.4	20.0	18.0	18.0	18.0	16.1
	Score	2250	2143	2143	2130	2116.5	2024.5	2020.5	2005.5	1562.5	1562.5	450.5	404	404	404	362
	Result No.		8	e	4	Ŋ	w	7	80	σ	10	11	12	13	14	15

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61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120

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1 NDVARGIVKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN

Sequence 199, Appl. Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (2, Appl.) Sequence (2, Appl.) Sequence (2, Appl.) Sequence (2, Appl.) Sequence (2, Appl.) Sequence (2, Appl.) Sequence (2, Appl.) Sequence (2, Appl.) Sequence (3, Appl.) Sequence (3, Appl.) Sequence (4, Appl.) Sequence (6, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.) Sequence (1, Appl.)	Length 434;	Indels 0; Gaps 0;
16 357 15.9 1079 14 US-10-112-488-39 17 349.5 15.5 1139 14 US-10-116-761-10856 18 359 15.1 1237 14 US-10-116-761-10856 19 316.5 13.2 1237 14 US-10-090-624-6 20 237.5 13.2 19725 15 US-10-084-8468-4 22 28.5 13.2 19725 15 US-10-084-8468-4 23 274 12.0 589 10 US-09-927-827-5 24 275 11.1 14 US-10-116-76-76-112934 25 26 11.8 110.1 14 US-10-116-76-76-12934 26 26 11.7 271 10 US-09-96-2918-2 29 260.5 11.6 271 10 US-09-96-2918-2 29 260.5 11.6 290 11.7 290 14 US-10-20-818-2 29 260.5 11.6 250 11.6 220-779-1344-5 29 260.5 11.6 269 11.5 271 14 US-10-242-549-56 25 25 11.5 271 14 US-10-242-549-6 25 257 11.4 269 9 US-09-975-116-49 257 11.4 269 9 US-09-975-116-49 257 11.4 269 9 US-09-975-116-49 257 11.4 269 10 US-09-975-116-49 257 11.4 269 10 US-09-975-116-49 257 11.4 269 11 US-10-075-895-1 257 11.4 269 11 US-10-075-895-1 257 11.4 269 11 US-10-075-895-1 257 11.4 269 14	ALIGNMENTS -689A-6 e 6, Application US/09985689A tion No. US20030022351A1 ANT: USACRATION: ANT: KARCHALA, YASUSHI ANT: RACKALA, YASUSHI ANT: RACKI, HENOVUKI ANT: SAFO, TSUYOSHI ANT: SAEXI, HENOVUKI ANT: SAEXI, KATSCHISA OF INVARITON: ALKALINE Proteases EPPERENCE: 215483US0 TT APPLICATION NUMBER: US/09/985,689A TT PLING DATE: 2002-07-01 APPLICATION NUMBER: JP P2000-355166 FILING DATE: 2001-11-22 APPLICATION NUMBER: JP P2001-114048 APPLICATION NUMBER: JP P2001	Similarity 100.0%; Pred. No. 3e-189; 4; Conservative 0; Mismatches 0;

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61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAXS 120
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                                                                                                          301 PSGNOGWGRVTLDKSLNVAPVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTSA 360
                                                                                                                                                                                                    SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
                                                                                                                                                                                                                                                                                       361 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
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TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
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                            241 WANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY
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95.2%; Score 2143; DB 15;
Best Local Similarity 93.5%; Pred. No. 7.9e-180;
Matches 406; Conservative 19; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10385662
| Sequence 2, Application US/10385662
| Publication No. US/0040002432A1
| GENERAL INFORMATION:
| APPLICANT: SOUTOA, NITSUYOSHI
| APPLICANT: SAITO, KAZUHIRO
| APPLICANT: SAITO, KAZUHIRO
| APPLICANT: SAITO, KAZUHIRO
| APPLICANT: SAITO, KAZUHIRO
| APPLICANT: SAITO, KAZUHIRO
| APPLICANT: SARI, KATGHIRSA
| APPLICANT: SARI, KATGHIRSA
| APPLICANT: NOMURA, MASHUMI
| APPLICANT: NOMURA, MASHUMI
| APPLICANT: NOMURA, MASHUMI
| TITLE OF INVENTION: Alkaline procease
| CURRENT APPLICATION NUMBER: US/10/385,662
| CURRENT FILING DATE: 2002-03-22
| PRIOR APPLICATION NUMBER: UP 2002-081428
| PRIOR APPLICATION NUMBER: UP 2002-165987
| PRIOR FILING DATE: 2002-10-18
| PRIOR APPLICATION NUMBER: UP 2002-304230
| PRIOR APPLICATION NUMBER: UP 2002-304231
| PRIOR PRILING DATE: 2002-10-18
| NUMBER OF SEQ ID NOS: 20
| SEQ ID NO 2
| LENGTH: 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Bacillus sp. KSM-KP43
US-10-385-662-2
                                                                                                                                                                                                                                                                                                                                                                                      421 VPVGPQTFSLAIVN 434
                                                                                                                                                                                                                                                                                                                                                            421 VPOGPOAFSLAIVN 434
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                                                                                              181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
                                                                                                                                                                                                                                                                                                                                                                      101 PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASISA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                     241 WANHDSKYAYWGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300
                                                                                                                                                                                                                                                                                                                                         301 PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                 SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
  61 NANDPNGHGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAXS 120
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                                                                                                                                                                                           181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                       121 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOS-09-98-5689A-1

SUBJECTION NO. US20030022351A1

GENERAL INFORMATION:

APPLICANT: HATADA, YUJI

APPLICANT: GGAWA, AKINORI

APPLICANT: SAFO, TSUYOSHI

APPLICANT: SAFO, TSUYOSHI

APPLICANT: SAFO, TSUYOSHI

APPLICANT: SAFAI, HISTOYUKI

APPLICANT: SAFAI, ALINOYUKI

APPLICANT: SAFAI, MISUYOSHI

APPLICANT: SOFEN, KASISHISA

TILE REFERENCE: 215483US0

CURRENT APPLICATION NUMBER: US/09/985,689A

CURRENT FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: JP P2001-114048

PRIOR APPLICATION NUMBER: JP P2001-114048

PRIOR APPLICATION NUMBER: JP P2001-114048

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 VPQGPQAFSLAIVN 434
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241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300
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                                                                                         300 PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA 359
301 PNGNQGWGRVTLDKSLNVAYVNESSALSTSQKATYTFTATAGKPLKISLVWSDAPASTTA 360
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                                                   361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
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12; Indels
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Sequence 7, Application US/09985689A

PUDLICANT: HATADA, YUJI

APPLICANT: AARADA, YUJI

APPLICANT: SAGEVAMA, YASUSHI

APPLICANT: SAGEVAMA, YASUSHI

APPLICANT: SAGEVAMA, YASUSHI

APPLICANT: SARI, HIROYUKI

APPLICANT: SUNTYOND, NOBUTUKI

APPLICANT: SUNTYOND, NOBUTUKI

APPLICANT: SAEKI, KATSUHISA

TILE OF INVENTION: ALRAINE protease8

FILE REFERNCE: 215483USO

CURRENT APPLICATION NUMBER: US/09/985,689A

CURRENT FILING DATE: 2002-07-01

FRIOR FILING DATE: 2000-11-22

FRIOR FILING DATE: 2000-11-2

FRIOR FILING DATE: 2001-04-12

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92.2%; Pred. No. 1.7e
iive 21; Mismatches
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Best Local Similarity
Matches 400; Conserva
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                                                                      241 WANHDSKYAYMGGISMAIPIVAGNVAQLREHFVKNRGIIPKPSLLKAALLAGAADIGLGY
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94.7%; Score 2130; DB 10;
Best Local Similarity 92.4%; Pred. No. 1.1e-178;
Matches 401; Conservative 24; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09985689A
Publication No US2003002351A1
GENERAL INFORMATION:
APPLICANT: MACRADA, YUJI
APPLICANT: MAGENAM, AKINORI
APPLICANT: MAGENAM, AKINORI
APPLICANT: MAGENAM, ANSUBHI
APPLICANT: MAGENAM, ANSUBHI
APPLICANT: SATO, TSUYCOSHI
APPLICANT: SATO, TSUYCOSHI
APPLICANT: SANITOM, NOBUTUKI
APPLICANT: SANITOM, AIKAINED
APPLICANT: SAEXI, KATSUHISA
ITILE OF INVENTION: AIKAINE PROCESSES
FILE REFERENCE: 215483US
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 2
LENGTH: 434
                                                                                                                                                                                                                                                                                                                                      VPQGPQAFSLAIVN 434
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ORGANISM: Bacillus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%; Score 2020.5; DB 10
88.2%; Pred. No. 4.7e-169;
live 28; Mismatches 22;
                                                                       APPLICANT: COGNA, AKINORI
APPLICANT: COGNA, AKINORI
APPLICANT: COGNA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUMITOWO, NOBUYUKI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483180
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT PELING DATE: 2002-07-01
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3.
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Publication No. US20030022351A1
GENERAL INPORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: OGAWA, AKINORI
APPLICANT: SAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
     Publication No. US20030022351A1
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Best Local Similarity 88.2%,
Matches 383; Conservative
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CORGANISM: Bacillus sp.
US-09-985-689A-3
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Best Local Similarity 88.5%; Pred. No. 2.1e-169;
Matches 384; Conservative 28; Mismatches 21;
                                                                                                                                                                                                                                           APPLICANT: HATADA, YUJI
APPLICANT: GGAWA, AKINORI
APPLICANT: SATO, TSUYGSHI
APPLICANT: SATO, TSUYGSHI
APPLICANT: SATO, TSUYGSHI
APPLICANT: SUNITOWO, NOBUYKI
APPLICANT: SUNITOWO, NOBUYKI
APPLICANT: SUNITOWO, ALKAINE APPLICANT: SAEKI, KATSUHISA
TITLE REPERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: UP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR APPLICATION NUMBER: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
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US-09-985-689A-3
; Sequence 3, Application US/09985689A
                                                                                                                                                                 Sequence 5, Application US/09985689A Publication No. US20030022351A1 GENERAL INFORMATION:
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420 VPVSPQTFSLAIVH 433
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ORGANISM: Bacillus sp
                                                                                                                                      -09-985-689A-5
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61 NANDPNGHGTHVVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Handlich:
APPLICANT: Bauditz, Peter K.
APPLICANT: Bauditz, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikelsen, Frank
TITLE OF INTENTION: Protease Variants And Compositions
FILE REFERENCE: 5435.200-US
CURRENT APPLICATION NUMBER: US/10/403,105
CURRENT FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: US/09/196,281A
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1332/97
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1332/97
PRIOR FILING DATE: BARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 345
                                                                                                                                                                       DB 14; Length 345;
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                                                                                                                                                                  Query Match 69.4%; Score 1562.5; DB 14; Best Local Similarity 92.5%; Pred. No. 6.6e-129; Matches 294; Conservative 16; Mismatches 7;
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, Sequence 13, Application US/10403105
; Publication No. US20030180933A1
; GENERAL INFORMATION:
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; LENGTH: 345
; TYPE: PRT
; ORGANISM: Bacillus
US-10-336-324-10
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US-10-403-105-13
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| Sequence 10, Application US/10336324
| Publication No. US20030176304A1
| September 10, Application No. US20030176304A1
| September 10, Application No. US20030176304A1
| APPLICANT: Handson, Peter APPLICANT: Mikkelsen, Frank APPLICANT: Mikkelsen, Frank APPLICANT: Mikkelsen, Frank TILIE OF INVENTION: Procease Variants and Compositions FILE REFERENCE: 5349.204-US
| CURRENT APPLICATION NUMBER: US/10/336,324
| CURRENT FILING DATE: 2003-01-03
| PRIOR PLILOATION NUMBER: US/09/512,251A
| PRIOR FILING DATE: 2000-02-24
| NUMBER OF SEQ ID NOS: 12
| SOFTWARE: PatentIn Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.6%; Pred. No. 9.8e-168;
Matches 380; Conservative 31; Mismatches 22;
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: OKUDA, MITSUTOSHI
APPLICANT: OKUDA, MITSUTOSHI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483US0
CURRENT PAPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR RILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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ORGANISM: Bacillus sp.
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US-10-336-324-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 GLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTNNAN-----DPNGHGTH
                                                                                                                                                                                                                                    APPLICANT: TAKAKURA, Hikaru
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: AKATO, Ikunoshin
TITLE OR INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPERENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: U5/10/090,624
CURRENT PILING DATE: 2002-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1997-06-10
PRIOR PLING DATE: 1997-06-10
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
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                                      518 KVVSY---KGAANYQVDVVS 534
       EVQAYNVPOGPQAFSLAIVN 434
                                                                                                                                                                    Sequence 1, Application US/10090624; Publication No. US20020132335A1; GENERAL INFORMATION:
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Publication No. US20020132335A1
GENERAL INFORMATION:
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Matches 131; Conservative
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                                                                          241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300
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148 AGARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 207
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Publication No. US20020132335A1

GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: TAKAKURA, Hikaru
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1997-06-10
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SSEQ ID NO 12
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20.0%; Score 450.5; DB 13; Length
Best Local Similarity 31.4%; Pred. No. 1.2e-30;
Matches 138; Conservative 69; Mismatches 170; Indels
                                                                                                                                                                                                                                         PSGNOGWGRVTLDKSLNV 318
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ORGANISM: Thermococcus celer
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US-10-090-624-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 SKYAYMGGISMAIPIVAGNVAQLREHFIKNRGIIP---KPSLLKAALIAGAIDIG-LGYP 301
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APPLICANT: MOSISHITA, Mio

APPLICANT: MASISHITA, Mio

APPLICANT: SAADA, Kiyozo

APPLICANT: SAADA, Kiyozo

APPLICANT: KATO, Iromoshin

ITILE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

FILER REFERENCE: TAKANURA-6

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT APPLICATION NUMBER: US/10/090,624

PRIOR PILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN Version 3.0

SEQ ID NO 4

LENGTH: 522
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Best Local Similarity 30.0%; Pred. No. 1e-26;
Matches 131; Conservative 63; Mismatches 168; Indels 7
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Publication No. US20020132335A1
GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, KYYOZO
APPLICANT: KATOZO
APPLICANT: KATOZO
APPLICANT: KATOZO
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (428)...(428)
; PHER INFORMATION: Xaa at position 428 is Gly or Val.
US-10-090-624-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 INLSLGSSQSSDGTDALSQAVNAAWDAGLVVVVAAGNSGPNKYTIGSPAAASKVITVGA- 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWANHD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 SKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITP---KPSLLKAALIAGATDIG-LGYP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 GLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTNNAN-----DPNGHGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 HINSWGAPVNGAYITDSRNVDDYVRKNDMAVLFAAGNEGFNGGIISAFGTAKNAITVGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GAGRVNAYKAINYDNYAKIVFTGYVANKGSQTHQFVISGASFVTATLYMDNAN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              18.0%; Score 404; DB 13; 30.0%; Pred. No. 1.4e-26;
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Publication No. USZ0030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SATRAK, TADAYOSHI
APPLICANT: APTICANT: WASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT FILE DEPLICATION NUMBER: US/10/156,761
CURRENT FILE OF SERENCE: 249-262
CURRENT FILE OF DEPLICATION NUMBER: US/10/156,761
CURRENT FILE OF DEPLICATION NUMBER: UP 2001-204089
PRIOR PLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR PLING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
CURRENT APPLICATION NUMBER: US/10/090,6.
CURRENT PILING DATE: 2002-03-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-0-06-10
PRIOR PILING DATE: 1999-0-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARR: PARCHIN VETSION 3.0
SEQ ID NO 16
LENGTH: 654
                                                                    US/10/090,624
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Best Local Similarity
Matches 131; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                   231 RSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAA-- 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 LIAGATDIGLGYPSGNQGWG-RVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 SLVWSDAPASTSASVTLVNDLDLVITAP----NGTKYVGNDFTAPYDNNWDGRNNVENVF 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519 SLAVRGAPAGVA---TLA---DTALTVPAHGTAATTVTGDGSKAPV-----GETSGQIV- 566
                                                                                                                                                                                                                                                  58 RINNANDPNGHGTHVAGSVLGNGTSN----KGMAPQANLVPQSVMDSNGGLGGLPSNVST 113
                                                                                                                                                                                                                                                                                                                      114 LFSQAYSAGARIHTNSWGAPVNGAYTTD--SRNVDDYVRKNDMAVLFAAGNEGPNGGTIS 171
                                                                                                                                                                              8 VKADVAQSS-----YGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALG 57
                                                                                                        Query Match 16.1%; Score 362; DB 14; Length 1208; Best Local Similarity 30.1%; Pred. No. 1.7e-22; Matches 135; Conservative 62; Mismatches 186; Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 INAPQSGTYTVEVQAYNVPQGPQAFSLAI 432
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; SEQ ID NO 13251
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13251
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Search completed: March 31, 2004, 16:34:02 Job time: 34.2177 secs

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31	332	3.4 3.5	36	3 G	w .	4.4 . ⊃ ⊟	42	43	44	4.5

	ALIGNMENTS
RESULT 1 118279 multidrug C; Species C; Date: 1 C; Accessi	resistance tran : Dictyostellum 5-Oct-1999 #sequ on: T18279
R;Shaulsky, G submitted to A;Reference r A;Accession: A;Status: pre	lsky, G.; Loomis, W.F. ted to the EMBL Data Library, June 1996 rence number: Z18855 ssion: T18779 us: preliminary; translated from GB/EMBL/DDBJ
	Molecule type: mRNA. Residues: 1-1743 <bha> Cross-references: BMBL:U60086; NID:g1399914; PID:g1399915; PIDN:AAB03331.1 Genetics: Gene: tagC</bha>
Query M Best Lo Matches	/ Match 23.0%; Score 518.5; DB 2; Length 1743; Local Similarity 28.0%; Pred. No. 6.3e-25; and 155; Conservative 77; Mismatches 155; Indels 193; Gaps 23.
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Ор	goilsiabrdiboshcresbskyripins
δ	69 GTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAY 119
qq	373 dTHICGSAAGTPEDSSVNISSFSGLATDAKIARFDLASGSSSLTPPSDLKQLYQPLY 429
ζ	120 SAGARIHTINSWGAFVINGAYITDSRNVDDYVRKN-DMAVLFAAGNEGPNGGIISA 172
qq	SID
à	173 PGTAKNAITVGATENLRPSFGSYADNI
οqα	487 OSTAKOVITVGAHQTIHENYLIDGPNYINYQSSVDINQELICDFDSRYCNYTTAQCCLES 546
ò	200
q _O	547 NATTGLASCCPTLLRKSVIDAANTQPLLYNENNICSFSSKGPTHDGRMKPALVAPGEYİT 606
ò	229 SARSSLAPDSSFWANHDSKYAYMGGTSWATPIVAGNVAQLREHF 272
QQ	607 SARSNGANTIDOCGDGSL-PNINALLA-ISGISMAISFAAAAITILRQXLVDGYYPIGSI 664
δ	273 IKNRGITPKPSLLKAALIAGATDIGLGYPSGNQGWGRVT 311
q	665 VESNKLOPIGSLLKALMINNAQLLNGTFQLITSSSITYPSNQVFENFAGASLVQGWGAIR 724
8	312 LDKSLNVAFVNETS338
qq	725 MSNWIHVYNNNNSNNNNKTSDGITKFDGIGGLDLRLVKFNQWKEESLSTGQNTSYCFTYK 784

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Abbush, intracellular alkaline serine proteinase aprX - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: Species:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
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15.3%; Score 344.5; DB 2;
Best Local Similarity 31.8%; Pred. No. 1.2e-14;
Matches 108; Conservative 45; Mismatches 98;
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Multidrug resistance protein - slime mold (DictyOstelium discoideum)

C;Dacei: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: THESET

R;Anusky, G: Kuspa, A.; Loomis, W.F.

Submitted to the EMBL Data Library, January 1995

A;Pescription: An MDR transporter/serine protease gene is required for prestalk speciality. A;Reference number: Z18850

A;Accession: TH8267

A;Accession: TH8267

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      ----AOSGKPLK---ISLVWSDAPASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYD 390
                                                              785 PSSSSSNSGNNIPRVVATLVWTDPPSYAGAKFNLVNNLDLTM----IYYRDNGSTIFYS 839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1905;
                                                                                                                                                                         840 NGGSSFLGLAPTODTLINNVEGIVENPTEPMTYRFMVAGTNVPMGPQNFS
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Matches 132; Conserv
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              A)Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13610.1; PID:e1183385; A)Experimental source: strain 168
C;Genetics:
C;Genetics:
C;Superfaully: subtilisin homology
F;146-398/Domain: subtilisin homology <SBT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 WCIQYNEDNPDEPIDIMSMSLGGDALRYDHEQEDPLVRAVEBAWSAGIVVCVAAGNSGPD 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILSARSSLAPDSSF----WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPK 281
                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                        49; Mismatches 120; Indels
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                                                                                                                                                                        14.4%; Score 324; DB 2; 31.6%; Pred. No. 2.4e-13;
                                                                                                                                                                                                                     Matches 106; Conservative
                                                                                                                                                                                                  Similarity
Residues: 1-442 <KUN>
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Best Local
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A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seroakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama keuchi, M.; Tamakoshi, A.; Tanamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yoshikawa, A; Authors: Yoshikawa, H.; Zumstein, B.; Yoshikawa, H.; Danchin, A.; A; Yeference number: A69580; MUID:98044033; PMID:9384377
A; Accession: D69730
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:299123; GB:AL009126; NID:92636240; PIDN:CAB15835.1; PID:92636344 A;Experimental source: strain 168 C;Comment: The amino terminal sequence of the mature protein and a molecular weight of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLAPDSSFWANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSL--LKAALI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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C;Species: Pyrococcus furiosus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 24-Oct-2000
C;Accession: T28159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DPRGEATDHGTHVAGTVAANGTI-KGVAPDATLLAYRVLGPGG--SGTTENVIAGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYGQGQVVAVADIGLDIGR--------NDSSMHEAFRGKITALYALGRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NANDPNG----HGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 REALSVGATOLPLNEYAVTFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGBAKDFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDLIGKVAVVKRGSIAFVDKADNAKKAGAIGMVVYNNLSGEIEANVPGMSVPTIKLSLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfemily: microbial serine proteinase vpr; subtilisin homology C;Reywords: hydrolase; serine proteinase [F1.28/Domain: signal sequence #status predicted <SIG>F1.29-160/Domain: propeptide #status predicted <PRO>F1.80-548/Domain: propeptide #status predicted <PRO>F1.80-548/Domain: subtilisin homology #status atypical <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |:| ||:| ||::
GYTGKGIKVAIIDTGVEYNHPDLKKNFGQYKGYDFVDNDYDPKETPTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%; Score 318.5; DB 2;
llarity 23.9%; Pred. No. 1.2e-12;
Conservative 53; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 KNAITVGATE----NLRPSFGSY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ADNI--
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450 MLSNEDGLKMRNELENGQNTVTFSIEFDKLVGETVADPSSRGPVMHTWMIKPDVSAPGVA 509
                                                                                                                                                                                                                                                                                                                                                                         KPGDFEGVDVEGKIALIVRGEIPFVEKAENAKAAGAVGAIIYNNVAGVQPTVPGLAIPTI 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALIAGATDI...-GLGYPSGNQG----------WGRVTLDKSLNVAF 320
                                                                                                                                                                                                                           DPNG----HGTHVAGSVLGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTL--FSQ 117
                                                                                                                                                                                                                                                                  678 GYYEGTIIVS------DGSQTVEVPTILFVSEPDYPRVTTFDLDENGVLFGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILSARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYTGEGITVAILDTGVDYTHPD------LVHAFGDYKGWDFIDNNDDPQETPPG
                                                                                                                                                                                                                                                                                                                                          AYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAISVGAT----RLPYNKYKASVFTSDGIDYPSADIMGFPSDEELLELDGETYEYAFAGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 IVSTIPTHQPDDPY-----GYGSRQGTSMASPHVAGAAALLLEAH-PNWGV----DHVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QHFTIHNLSNKRKTYQFDVQFAGNPDGIKVKTSKNLRVQPGKTQ-KINFNVQVDARKLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NGTKYVGNDFTAPYDNNWDGRNNVE---NVFINA---PQSGTYTVEV----QA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 VNETSSLSTNOKATYSFTAQ-SGKP----LKISLVWSDAPASTSASVTLVNDLDLVITAP
                                                                                                               GLYGOGOVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGR------TINN-
12.9%; Score 291; DB 2; Length 79 clarity 24.1%; Pred. No. 6.8e-11; Conservative 57; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAITVGATENLRPSFGSY-----ADNINH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNVPOGPQAFSLAI 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y-LPNGAEEFGLWI 739
                                 Local Similarity
les 148; Conserv
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      Query Match
Best Local S
Matches 148
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000

A;Trile: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: G83753

A;Accession: G83753

A;Residues: 1-799 <STO>
A;Residues: 1-799 <STO>
A;Residues: 1-799 <STO>
A;Coss-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04550.1; GSPDB:GNOG A;Experimental source: strain C-125
C;Genetics:
A;Genetics:
oorhorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, R.J.; Vos, J. Biol. Chem. 271, 20426-20431, 1996
A.Title: Isolation and characterization of the hyperthermostable serine protease, pyroly A.Reference number: Z20481; MUID:9635370; PMID:8702780
A.Accession: T28159
A.Accession: T28159
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A.Accession: T28159
A.Accession: T28159
A.Accession: DAA
A.Residues: 1-1398
A.Coss-references: EMBL:U55835; NID:g1556462; PID:g1556463; PIDN:AAB09761.1
A.Resperimental source: DSM3638
C.Genetics:
A.Genetics:
A.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGARIHTNSWG--APVNGAYTTDSR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 NVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSFGSYAD----- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------NINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWANHD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 YPSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              532 DYYGFYYFPAYTWV-RIAFFSSRGPRIDGEIKPNVVAPGYGIYSSLPMWIGGADF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDI-----GLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SMHEAFRGKITAIYALGRTNNANDPN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GHGTHVAGSVLGNGTSN------KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAPGAQIMAIRVLRSDG--RGSMWDIIEGMTYAATHGADVISMSLGGNAPYLDGTDPESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                127;
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;Superfamily: microbial serine proteinase vpr; subtilisin homology
;Keywords: hydrolase; serine proteinase
;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                       Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 314.5; DB 2; 27.9%; Pred. No. 4.6e-12; tive 50; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 A---SVILVNDLDLVITAPN----GIKYVGN 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GOGOVVAVADTGLDTGRNDS----
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.9%
Matches 126; Conservative
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--VAQFSSRGPT-KDGRIKPDVMAPGTF

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A;Status: preliminary
A;Solecule type: DNA
A;Rolecule type: DNA
A;Rossiques: 1-715 <TSU>
A;Cross-references: DDBJ:D28600; NID:g1536787; PIDN:BAA18912.1; PID:d1019647; PID:g2160
A;Cross-references: strain 0-7
C;Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sens
C;Genetics:
alkaline serine proteinase (EC 3.4.-.-) I precursor - Alteromonas sp.
NiAlternate names: sutilase
C.Species: Alteromonas sp.
C.Species: Alteromonas sp.
C.Accession: JC4908
R;Tsujibo, H.; Miyamoto, K.; Tanaka, K.; Kaidzu, Y.; Imada, C.; Okami, Y.; Inamori, Y.
Biosci. Biotechnol. Blochem. 60, 1284-1288, 1996
A,Title: Cloning and sequence analysis of a protease-encoding gene from the marine bact A;Reference number: JC4908; MUID:97141200; PMID:8987544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Superfaily: subtilisin homology
C.Keywords: hydrolase
F1.40/Domain: signal sequence #status predicted <SIG>
F,41-150/Domain: andino-terminal propeptide #status predicted
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F;151-496/Product: alkaline serine protease I #status predicted <wat> F;182-452/Domain: subtiliar, homology < SBT> F;497-715/Domain: subtiliar, homology < SBT> F;497-715/Domain: carboxyl-terminal propeptide #status predicted <ctp> F;239-294,335-372,478-481/Disulfide bonds: #status predicted <ctp> F;239-294,335-372,478-481/Disulfide bonds: #status predicted <ctp> Cuery Match Query Match 12.4%; Score 279; DB 2; Length 715; Best Local Similarity 25.9%; Pred. No. 3.4e-10; Matches 124; Conservative 51; Mismatches 168; Indels 136; Gaps 22; Qy 21 GQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTNNANDP</ctp></ctp></ctp></wat>	Db 228 GIPPAASSSWHGTHVAGTVAAVTNNTTGVAGTAXGAKVVPRVLGKCGGSLSDIADAIVWA 287 104LGGLPSNVSTLFSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVL 157 28 SGGTVSGIPANANPAEVINMSLGGGGSCSTTMQNA-INGAVSRGTTVV 334 158 FAAGNEGPNGGTISAPGTAKMAITVAGATENLRPSGSADNINHVAQFSSRGFTKDGR 215 335 VAAGNDASNVSG-SLPANCANVIAVAATTSAGAKASYSNFGTGI
270	RESULT 10 surface layer-associated STABLE proteinase - Staphylothermus marinus surface layer-associated STABLE proteinase - Staphylothermus marinus NyAlternate names: hyperthermostable proteinase C;Species: Staphylothermus marinus C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C;Accession: T29090 R;Mayr, J; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J. Curr. Biol. 6, 739-749, 1996 A;Title: A, hyperthermostable protease of the subtilisin family bound to the surface lay A;Accession: T29090 A;Accession: T29090 A;Accession: preliminary; translated from GB/EMBL/DDBJ
RESULT 9 S11890 Series proteinase (EC 3.4.21) precursor, extracellular - Xanthomonas campestris pv. ca N;Alternate names: subtilisin-related proteinase C;Species: Xanthomonas campestris pv. campestris C;Actession: S11890 C;Actession: S11890 C;Actession: S11890 C;Actession: S11890 C;Actession: S11890 C;Actession: S11890 C;Actession: S11890 A;Title: A multipurpose broad host range cloning vector and its use to characterise an A;Reference number: S11890; MUD: 90251253; PMID: 2187155 A;Actession: S11890 A;Molecule type: DNA A;Reference number: S11890; MUD: 90251253; PMID: 2187155 A;Actession: S1189 A;Molecule type: DNA A;Residues: 1-580 club A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S1189 A;Actession: S11819 A;Actess	Aprolection by Paragrams Approaches that Approaches the Approaches that Approaches the Approaches that Approaches the Approaches that Approaches the Approaches that Approaches the Approaches the Approaches the Approaches the Approaches the Approaches the Approaches the Approaches the Approach to the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach the Approach to Approach the Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approach the Approach to Approac
Query Match 12.2%; Score 274; DB 2; Length 580; Best Local Similarity 27.7%; Pred. No. 5.4e-10; Matches 130; Conservative 53; Mismatches 157; Indels 130; Gaps 25; Oy 21 GOGOVAVADTGLDTGRNDSSMHEAFRGKITAIVALGRTNNAND	Db 547 GSIYINFWLQQFPGIDYRSSFMDEILAİRİYİ İİİİİİİİİİİİİİİİİİİİİİİİİİİİİİİİİ

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subtilisin-type proteinase (EC 3.4.21.-) BH3763 precursor [similarity] - Bacillus halod C;Species: Bacillus halodurans C;Species: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: C84120 C;Accession: C84120 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: C84120 A;Status: preliminary
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A;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 MSLGSSGESSLITNAVN---YSYNKGVLIJAAAGNSGPYQGSIGYPGALVNAVAVAAALEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 -SWGAPVNGAYTIDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAITVGATEN
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     -references: EMBL:X62369; NID:g40200; PIDN:CAA44227.1; PID:g40201
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(Superfamily: subtilisin; subtilisin homology

(Skeywords: extracellular protein; hydrolase; serine proteinase

(Skeywords: extracellular protein; hydrolase; serine proteinase

F;1-23/Domain: signal sequence #status predicted <BIO>

F;11-411/Domain: proteinase #status predicted <MAT>

F;136-374/Domain: subtilisin homology <BI>

F;145,185,360/Active site: Asp, His, Ser #status predicted
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                                                                                                                                                                                                                                                                                    Length 420;
                                                                                                                                                                                                                                                                               12.1%; Score 272; DB 1; Length 42 30.4%; Pred. No. 4.7e-10; ive 41; Mismatches 123; Indels
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llarity 24.2%; Pred. No. 1.3e-09;
Conservative 48; Mismatches 159;
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AGYGDDFASGFGFATV 419
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Matches 127; Conserv
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A;Molecule type: DNA
A;Residues: 1-757 <STO>
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Best Local Simil
Matches 96; (
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R;Davail, S.; Feller, G.; Narinx, E.; Gerday, C.
Gene 119, 143-144, 1992
A;Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillu A;Reference number: S25835; MUD:93012966; PMID:1398082
A;Accession: S25835
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ATDIGLGYPSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWS 352
                                                      -WLAYVSEGIQEAFLENYYT 766
                                                                                                         -DFTAPYDNN 392
                                                                                                                                                  DFGPYIGYVLPYLADTDYYGVVKPGSSKNFTLNIVGNGAVSLSAWNTVLYKEYTV-YDGV 825
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C)Species: Bacillus sp.
C)Becies: Bacillus sp.
C)Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999
C)Accession: S23407
B)Narinx, E.; Davail, S, Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1131, 111-113, 1992
A)Atitle: Nucleotide and derived amino add sequence of the subtilisin from the A)Atitle: Nucleotide and derived amino add sequence of the subtilisin from the A)Accession: S23407, MVID:92256481; PMID:1581352
A)Andlecule type: DNA
A)Residues: 1-420 <NAR>
                                                                                                                                                                                                                                                                                                                                                                             ibtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)
Species: Bacillus sp.
Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGESSLIT---NAVDYAYDKGVLIIAAAGNSGFKEGSIGYFGALVNAVAAALENTIQN-
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A,Residues: 1-419 <DAV>
A;Cross-references: EMBL:X63533; NID:g40198; PIDN:CAA45096.1; PID:g40199
A;Cross-references: EMBL:X63533; NID:g40198; PIDN:CAA45096.1; PID:g40199
C;Superfamily: subtilish; subtilish; bromology
C;Keywords: extracellular protein; hydrolase; serine proteinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;2-110/Domain: propeptide #status predicted <PRO>
F;111-419/Product: microbial serine proteinase #status predicted <MAT>
F;135-373/Domain: subtilish homology <SBT>
F;144,184,359/Active site: Asp, His, Ser #status predicted
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                                                                                                 DAPASTSASVTLVNDLDLV-ITAPNGTK----YVGN-
                                   AKDI--WYPAFSQGSGRVDALKAADTVFISE-
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Best Local Similarity
Matches 83; Conserv
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293
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OY 118 AYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNBGPNGGTISAPGTAK 177 DD 228 AVEDGVDVINLSLGNTVNGFDWPTSLALDAAVEEGVVAVT-SNGNSGPNMMTVGSFGTSK 286	RESULT 15 A35742 aqualysin (BC 3.4.21) I precursor - Thermus aquaticus C;Species: Thermus aquaticus
OY 178 NAITVGAT194 DD 287 KAISVGASAPPLNTPYLTAFGEBNEISLYPFSGGLPWAFKRDLPMIDVGYGTEKEWEGVD 346	C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: A35742; S00620; S00324 R;Terada, I.; Kwon, S:T.; Miyata, Y.; Matsuzawa, H.; Ohta, T. J. Biol. Chem. 265, 6576-6581, 1990
195YADNINH	A;Title: Unique precursor structure of an extracellular protease, aqualysin I, with NH- A;Reference number: A35742; MUID:90216674; PMID:2182621 A;Accession: A35742
347 ABGKVVLIKRGMVPFTEKVMHAVAARARGVIIYNNTPGPFTGMIEGGVNIPVVSITREDG 202	A; Molecule type: DNA A; Residues: 1-513 <ter> A; Cross-ferences: GB:J90108; GB:D90108; GB:J05414; NID:9217171; PIDN:BAA14135.1; PID: A; Note: the authors translated the codon CTG for residue 470 as Val, and GGT for residu</ter>
EFLLEQLELQKNKELTLRTIYRKEEDFVALFSSRGPVTHTWDVKPDVVAPGVSIDS LAPDSSFWANHDSKYAYMGGTSWATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGA	R,Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T. Bur. J. Blochem. 173, 491-497, 198 A;Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline serin A;Reference number: S00620; MUID:88225062; PMID:3286255
OY 294 TDIGLGYPSGNQSWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGRPLKISL 349 CY 101GLGYPSGNQSWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGRPLKISL 349 CONTRACTOR OF THE CONTRACTOR OF	A;Accession: SUD&ZU A;Molecule type: DNA A;Rolduge: 75-442 <kwo> A;Residuge: 75-442 <kwo> A;Cross-references: EYBL:X07734; NID:g48069; PIDN:CAA30559.1; PID:g602091 A;Note: part of this sequence, including the amino and carboxyl ends of the mature prot</kwo></kwo>
QY 350 UWSDAPASTSASVTL-UNDLDLVITAPNGTKYVGNDFTAPYDNNW 393	R;Matsuzawa, H.; Tokugawa, K.; Hamaoki, M.; Mizoguchi, M.; Taguchi, H.; Terada, I.; Kwo: Bur. J. Biochem. 171, 441-447, 1988 A;Title: Purification and characterization of aqualysin I (a thermophilic alkaline seri: A;Reference number: S00324; MUID:88151937; PMID:3162211
RESULT 14 139974 139974 139974 139974 139974 139974 139974 139974 139974 139974 139974 139974 139974 139974 139974 139974 139976 139977	A,Accassion: \$00324 A,Molecule type: protein A,Residues: 128-170 <amats> C,Superfamily: subtilisin; subtilisin homology C,Superfamily: subtilisin; subtilisin bedicted <813> C,Keywords: extracellular protein; hydrolase; serine proteinase F,1-14/Domain: storeptide #status predicted <813> F,15-14/Domain: propeptide #status predicted <rgs- #status="" <88t="" <ats-="" aqualysin="" domain:="" experimental="" f,128-408="" f,155-364="" homology="" product:="" subtilisin="" =""> F,155-257, 281-283/Argdion: SI specificity or crevice #status predicted F,409-513/Domain: carboxyl-terminal propeptide #status predicted <cfr> F,166,197,349/Active site: Asp, His, Ser #status predicted</cfr></rgs-></amats>
A.Accession: 139974 A.Accession: 139974 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Status: preliminary; translated from GB/EMBL/DDBJ A.Rosidues: 1-401 <res- <rsp-="" a.cross-references:="" c.superfamily:="" domain:="" f.151-361="" gb:l29506;="" homology="" nid:9529979;="" pid:9529980="" pidn:aaa63688.1;="" subtilisin="" subtilisin;=""></res->	Query Match Best Local Similarity 28.2%; Pred. No. 3.3e-09; Matches 122; Conservative 43; Mismatches 157; Indels 111; Gaps 23; Qy 16 SYGLYGQGQVVAVADIGLDIGRNDSSMHBAFRGKITALY-ALGRINNANDPNGHGTHVAG 74
Query Match 11.8%; Score 264.5; DB 2; Length 401; Best Local Similarity 32.6%; Pred. No. 1.3e-09; Matches 86; Conservative 28; Mismatches 95; Indels 55; Gaps 11;	Db 152 TYTATGRGVNVTVÍDÍTGIRÍTHREFGGRARVGYDÁLG-GNGQDCNGHGTHVÁG 203 Qy 75 SYLGNGTBNKGMAPQANLVFGSVMDSNGGLGELPBNVSTLFSQAYSAGARIHTNSWGAP-133 1 :
11 DVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHBAFRGKITALYALGRTNNANDFNG 67	134VNGAYTIDSRNVDDYVRKXDMAVLFAAGNEGPNGGIISAPGTAKNAITVGA
6 HGIHVAGSVLGNGISNKSMAPQANIVFQSYMDSNGGLGGLPSNVSTLFSQAYBAGAR 12 193 HGIHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNGSGTLSDIADAIIYAADSGAE 25	QY 185 TENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTFILSARSSLAPDSSFWA 242
	QY 243 NHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITFKPSLLKAALIAGATDIG 297
306VDQYDRLASFSNYGTW	QY 298 LGYPSGNOGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISL 349
DD 338 -NRYAYMSGTSMASPHVAGLAALL 360	OY 350 VWSDAPASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAP 407 Db 447 AWLRGPAGTDFDLYLWRWDGSRWLTVGSS-TGPTSEBSLSYSG 488

Sat Apr 3 17:20:10 2004

\$ 8

Search completed: March 31, 2004, 16:10:22 Job time : 13.3508 secs

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March 31, 2004, 15:58:03; Search time 7.51154 Seconds (without alignments) 3008.498 Million cell updates/sec
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-985-689A-6 2250 1 NDVARGIVKADVAQSSYGLY.......EVQAYNVPQGPQAFSLAIVN 434 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

141681 Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q23868 dictyosteli	P54683 dictyosteli	P29141 bacillus su			bacillus s	bacillus	thermus ad	bacillus	bacillus	bacillus	bacillus	bacillus	vibrio a	bacillus	bacillus	P29140 bacillus cl	bacillus	P00782 bacillus am	P58099 streptococc	P00781 bacillus li	P04189 bacillus su	P20724 bacillus sp	P07518 bacillus pu	P15926 streptococc	P00783 bacillus su	P29142 bacillus st	P29118 cephalospor	Ω	P29143 halophilic	bacillus	P04072 thermoactin	-
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ALIGNMENTS

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                                                                            ----AQSGKPLK---ISLVWSDAPASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYD 390
                                                                                                      785 PSSSSSNSGNNIPRVVATLVWTDPPSYAGAKFNLVNNLDLTM-----IYYRDNGSTIFYS 839
665 VESNKLQPTGSLLKALMINNAQLLNGTFQLITSSITYPSNQVFENFAGASLVQGWGAIR 724
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PROSITE; PS0021; ABC_IMAPORTER 1; 1.
PROSITE; PS00131; ABC_TRANSPORTER 2; 1.
PROSITE; PS00136; SUBTILASE ASF; FALSE NEG.
PROSITE; PS00137; SUBTILASE ASF; FALSE NEG.
PROSITE; PS00137; SUBTILASE FIS; 1.
PROSITE; PS00138; SUBTILASE FIS; 1.
Hydrolase; Serine protease; ATF-binding; Transport; Transmembrane; Signal.
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                                                                                                                                 N------NWDGRNNVENVFINAPQSGTYTVEVQAYNVPQGPQAFS 429
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01-OCT-1996 (Rel. 34, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagB precursor (BC 3.4.21.-).
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
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InterPro; IPR00649; ABC_Tmenbrane; I.Pfam; PP00665; ABC_Tmenbrane; I.Pfam; PP00069; ABC_Tran; I.Pfam; PP000009; ABC_Tran; I.Prophom; PRNUTS; SUBTILISIN.
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                                                 -LKISLVWSDAPASTSASVTLVNDLDL-----VITAPN--GTKYVGNDFTAPYDNN
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 161-195.
MEDLINE-92041574; PubMed-1938892;
Sloma A., Rufo G.A. Jr., Theriault K.A., Dwyer M., Wilson S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of the gene for an additional extracellular serine protease of Bacillus subtilis."; J. Bacteriol. 173:6889-6895(1991).
                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor extracellular protesse vpr precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                         Sacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                429
                                                                                                                393 WDGRNNVENVFINAPQSGTYTVEVQAYNVPQGPQAFS
                                                                                                                                   - DTLNNVEGIIINPTKAMNYKFTIAGTNVPIGPOKFS
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MEDLINE=98044033; PubMed=9384377;
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Bacillus subtilis.
                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 LYGQGQVVAVADIGLDIGR---NDS----SMHEAFRGKITALYALGRINNANDP--N
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PRESTALK-SPECIFIC PROTEIN TAGB.
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ive 72; Mismatches 162; Indels
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Matches 163; Conserv
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 RAVQDGADVMULSLGNSLNNPDWATSTAL-DWAMSEGVVAVTSNGNSGPNGWTVGSPGTS 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GLYGQGQVVAVADTGLDTGR--------NDSSMHEAFRGKITAIYALGRTN 60
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REAISVGATQLPLNEYAVTFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKDFBG
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GYTGKGIKVAIIDTGVEYNHPDLKKNFGQYKGYDFVDNDYDPKETPTG-------
  Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Mismatches 155; Indels 213; Gaps
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(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                             Nature 390:249-256(1997).

-i FUNCTION: NOT REQUIRED FOR GROWTH OR SPORULATION.
-i SUBCELLULAR LOCATION: Secreted.
-i FUNCELLULAR UNDERGOES C-TERMINAL PROCESSING OR PROTEOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 318.5; DB 1; Length 806; Pred. No. 5.3e-13;
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    -!- SIMILARITY: Belongs to peptidase family S8.

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Interpro; PR003137; PA.
Interpro; IPR000209; Peptidase S8.
Interpro; IPR009020; Protease_Inhib.
                                                                                                                                                                                                                                                                                                                                               EMBL; M75590; AAA22881.1; -.
EMBL; X73124; CAA51601.1; -.
EMBL; Z99123; CAB15835.1; -.
PIR; A41341; A41341.
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806 AA;
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                                                                                                            619
                                                                                                                                                                                                                        959
                                                      291 AGATDI----GLGYPSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLK 346
THDPD-----HPYGYGSKQGTSMASPHIAGAVAVIKQ-----AKPKWSVEQIKAAIM 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and characterization of the hyperthermostable serine procease, pyrolysin, and its gene from the hyperthermophilic archaeon Pyrococcus furiosus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: Glycosylated.
-!- MISCELLANEOUS: Thermostable; high activity at 95 degrees Celsius.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                      565 NTAVTLKDSDGEVYPHNAQGAGSARI---MA--IKADSLVSPGSYSYGTFLKENGNETK
                                                                                                                                                                                                            347 ISLVWSDAPASTSASVTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDG--RNNVENVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A., SEQUENCE OF 150-184, AND CHARACTERIZATION.
STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=96355370; PubMed=8702780;
Voorhorst W.G.B., Eggen R.I.L., Geerling A.C.M., Platteeuw C., Siezen R.J., de Vos W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-00T-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Pyrolysin precursor (EC 3.4.21.-).
PLS OR PF0287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1398 AA.
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PIR; T28159; T28159.
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                                                                                                                                                                                                                                                                                                                                          657 РАНОТСКАТАКУК 669
                                                                                                                                                                                                                                                                                       405 NAPOSGTYTVEVQ 417
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NCBI_TaxID=2261;
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SEQUENCE STRAIN-ATCC 33913 / NCPPB 528;

XX MEDLINE-20202145; PubMed-12024217;

XA da Silva A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.;

Alves L.M.C., do Amaral A.M.; Bertolini M.C.; Camargo L.B.A.;

Alves L.M.C., do Amaral A.M.; Bertolini M.C.; Camargo L.B.A.;

Ansarotte G.; Cannavan F.; Cardozo J.; Chambergo F.; Ciapina L.P.;

An Cicarelli R.M.B.; Coutlinfo L.L.; Cursino-Santos J.R.; El-Dorry H.;

Raria J.B.; Ferreira A.J.S.; Ferreira R.C.C.; Ferro M.I.T.;

Rarian B.C.; Machado M.A.; Madeira A.M.B.N.; Martinez-Rossi N.M.;

Antins E.C.; Machadus G.M.; Menck C.F.M.; Miyaki C.Y.; Moon D.H.;

Ratins E.C.; Machadus J.M.; Newa V.K.; Oliveira M.C.; Oliveira V.R.;

Pereira H.A.; Rossi A., Sena J.A.D.; Silva C.; de Souza R.F.;

Spinola L.M.; Novo M.T.M.; Okuru V.K.; Oliveira M.C.; Oliveira V.R.;

A prindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;

Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;

Trindade dos Comparison of the genomes of two Xanthomonas pathogens with differing
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                                                                   ----MSGTSMATPHVSGVVALLISG-AKAEGIYYNPDIIKKVLESGATWLEGDPYTGQK 639
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                    246 SKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDI-----GLG
                                                                                                                    300 YPSGNOGWGRVTLDKSLNVAFVNETSSLSTNOKATYSFTAQSGKPLKISLVWSDAPASTS
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Nature 417:459-463(2002).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to peptidase family S8.
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01-NOV-1991 (Rel. 20, Last sequence update)
01-REB-2003 (Rel. 41, Last amotation update)
Extracellular protease precursor (EC 3.4.21.-)
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PIR, S11890, S11890.
HSSP, P00782, 2SBT.
MEROPS, S08.UPA, -
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               MEROPS 3.08 100; --.
MEROPS 3.08 100; --.
InterPro; IPR000209; Per
InterPro; IPR0002080; Per
Fam; PF00082; Peptidase_S8; 1.
PERM; PF00082; Peptidase_S8; 1.
PROSTIE; PF00073; SUBTILASE_ASP; 1.
PROSTIE; PS00136; SUBTILASE_HIS; 1.
PROSTIE; PS00138; SUBTILASE_HIS; 1.
PROSTIE; PS00138; SUBTILASE_HIS; 1.
PROSTIE; PS00138; SUBTILASE_HIS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 SGGTVSGIPANANPAEVINMSLGGGGSCSTTMQNA-INGAVSRGT------TVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 IKPDVMAPGTFILSARSS--LAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DVSAPGSSILSTLNSGTTTPGS-----ASYASYNGTSMASPHVAGVVALVQS--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GOGGVVAVADIGL----DIGRNDSSMHEAFRGKITAIYALGRINNAND------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSGTVVAVIDTGITSHADLNANILAGYDFISDATTARDGNGRDSNAADEGDWYAANECGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 GIPAASSSWHGTHVAGTVAAVTNNTTGVAGTAYGAKVVPVRVLGKCGGSLSDIADAIVWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LGGLPSNV--STLFSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAAGNEGPNGGTISAFGTAKNAITVGATEN -- LRPSFGSYADNINHVAQFSSRGFTKDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 KNRGITPK--PSLLK--AALIAGAIDIGLGYPSGNOGWGRVTLDKSLNVAFVNETS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSASVTLV----NDLDLVI---TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGNTLTNGTPVTGLGAATGAELNYTIT---VPAG-SGTLTVTTSGGSGDADLYVRAGSA
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SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPOSGTYTVEVQAYNVPQG 424
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Interbro; IPR000209; Peptidase_S8.
Interbro; IPR007280; PFC.
Interbro; PR009020; Protease_inhib.
Pfam; PR009021; Protease_inhib.
Pfam; PR04151; PPC; 1.
PRNO1751; SR00123; SUBTILISIN.
PROSITE; PS00135; SUBTILIASE_ASP; 1.
PROSITE; PS00137; SUBTILIASE_ASP; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=29336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8C9A2CAE4E7F47CB CRC64;
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DC-2003 (Rel. 42, Last annotation update)
Subtilisin precursor (EC 3.4.21.62).
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SEQUENCE FROM N.A.
MEDLINE=92256481; Pubmed=1581352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.7
Matches 130; Conservative
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450
580 AA;
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DISULFID
SEQUENCE
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"Nucleotide and derived amino acid sequence of the subtilisin from
The anteractic psychrotroph Bacillus TA39.";

Elochim. Blophys. Acta 1131:111-113(1992).

Elochim. Blophys. Acta 1131:111-113(1992).

I catalyzes the hydrolysis of proteins and peptide amides.

I catalyzes the hydrolysis of proteins with broad specificity

C -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C -!- COFACTOR: Binds 1 calcium ion per subunit (Potential).

C -!- SUBCELLUANEOUS: Sereted

C -!- SUBCELLUANEOUS: Sereted

C -!- ALSCELLANEOUS: Secretion of subtilisy is associated with onset of sporulation, and many mutations which block sporulation at early stages affect expression levels of subtilishin However, subtilishin is not necessary for normal sporulation.
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 ALADGGTGNGVYGVAPDADLWAYKVLGDDG~~SGYADDIAAAIRHAGDQATALNTKVVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGINIAVLDTGVNTN------HPDLRNNVBQCKDFTVGTTYTNNSCTDRQGHGTHVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VL---GNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGARIHTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAITVGATEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 MSLGSSGESSLITNAVN---YSYNKGVLIIAAAGNSGPYQGSIGYPGALVNAVAALEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 LRPSFGSYADNINHVAQFSSRGPT-KDG-----RIKPDVMAPGTFILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ANHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOGOVVAVADTGLDTGRNDSSMHEAFRGKITAI--YALGRT---NNANDPNGHGTHVAGS
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(BY SIMILARITY).
(BY SIMILARITY).
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PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_ERS; 1.
Hydrolase; Sporulation; Serine protease; Zymogen; Metal-binding; Calcium-binding; Signal.
SIGNAL 1.26
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SUBTILISIN.
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CHARGE RELAY SYSTEM (BY SIM
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CALCIUM (POTENTIAL).
W. AE4F121BD32E26EC CRC64;
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30.4%; Pred. No. 2.1e-10;
''' Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000209; Peptidase S8.
Pfam; PF00082; Peptidase S8; 1.
PRINTS; PR00723; SUBTILISIN.
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44086 MW;
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HSSP; Q99405; 1MPT.
MEROPS; S08.UPA; -.
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11 DVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTNNANDP---NG
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CALCIUM 3.
CALCIUM 1.
CALCIUM 1 (VIA CARBONYL OXYGEN).
CALCIUM 1 (VIA CARBONYL OXYGEN).
SODIUM (VIA CARBONYL OXYGEN).
SODIUM (VIA CARBONYL OXYGEN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 264.5; DB 1;
ilarity 32.6%; Pred. No. 5.9e-10;
Conservative 28; Mismatches 95;
 Ouery Match
Best Local Similarity
Matches 86; Conserv
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146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Therepro; IPRO00229; Peptidase S8.

InterPro; IPRO00229; Protease Inhib.

Professe Inhib.

Professe Inhib.

Professe Inhib.

PRINTS; PR00123; SUBTILASE S8; I.

PROSITE; PS00136; SUBTILASE ASP; I.

PROSITE; PS00136; SUBTILASE ASP; I.

PROSITE; PS00139; SUBTILASE SER; I.

PROSITE; PS00139; SUBTILASE SER; I.

PROSITE; PS00139; SUBTILASE SER; I.

PROSITE; PS00139; SUBTILASE SER; I.

THAN 122 POTENTIAL.

PROPER 25 121 THERMOPHILIC SERINE PROTEINASE.

THAN 122 A01 THERMOPHILIC SERINE PROTEINASE.

THAN 122 A01 THERMOPHILIC SERINE PROTEINASE.

THAN 124 A01 SERIAS SYSTEM.

THAN 125 A01 CHARGE RELAY SYSTEM.

THAN 126 126 CALCIUM I.
                                                                                                                                                                                                                                    MEDLINE=20057863; PubMed=10588904;

MEDLINE=20057863; PubMed=10588904;

Smith C.A., Toogood H.S., Baker H.M., Daniel R.M., Baker E.N.;

Calcium-mediated thermostability in the subtilisin superfamily: the crystal structure of Bacillus Ak.1 protease at 1.8-A resolution.";

J. Mol. Biol. 294:1027-1040(1999).

-! COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

-! SUBCELIULAR LOCATION: Secreted.

-! MISCELIANBOUG: Has a pH optimum of 8.5, a temperature optimum of
                                                                                                                                                                        MEDLINE-95085262; PubMed-7993087;
Maciver B., McHale R.H., Saul D.J., Bergquist P.L.;
"Cloning and sequencing of a serine proteinase gene from a
thermophilic Bacillus species and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THERMOPHILIC SERINE PROTEINASE.
CHARGE RELAY SYSTEM.
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CALCIUM 1.
                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thermophilic serine proteinase precursor (EC 3.4.21.-) (Ak.1
                                                                                                                           Bacillus sp. (strain AKI).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                      75 degrees Celaius.
                                                                                                                                                                                                             coli.";
Appl. Environ. Microbiol. 60:3981-3988(1994)
                                                                401 AA
                                                                PRT;
            : | |: | : | 404 AGYGDDFASGFGFATV 419
 SG----NQGWGRVTL 312
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                                                                STANDARD;
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PDB; 1DBI; 18-NOV-99.
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=1409;
                                                               THES BACSP
045670;
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RA MEDELINE-88151937; PubMed=3162211;

RA Terada I., Kwon S.-T., Ohta T.;

A Terada I., Kwon S.-T., Ohta T.;

Terada I., Kwon S.-T., Ohta T.;

Terada I., Kwon S.-T., Ohta T.;

RT "Purification and characterization of aqualysin I (a thermophilic alkaline serine protease) produced by Thermus aquaticus YT-1.";

Eur. J. Biochem. 171:441-447(1981).

The optimal temperature for its caseinolytic activity is 80 degrees Celsius.

The optimal temperature for its caseinolytic activity is 80 degrees Celsius.

The optimal temperature for its caseinolytic activity is 80 degrees Celsius.

The OPTIMAL STAGE: Secreted from the early stationary phase contil the time the cells cease to grow.

Until the time the cells cease to grow.

The PROTEOLYTIC ACTIVITY OF AQUALYSIN I ITSELF, IN THAT ORDER. THE COTEMINAL PRO-SEQUENCES ARE REMOVED THROUGH THE COTEMINAL PRO-SEQUENCES OR TRANSLOCATION OF THE PROTEOLYTIC ACTIVITY OF AQUALYSIN I ITSELF, IN THAT ORDER. THE COTES THE OUTER MENBRANE.

C-TERMINAL PRO-SEQUENCE IS REQUIRED FOR TRANSLOCATION OF THE PROTEOLYTIC ACTIVITY OF AQUALYSIN I IS produced through a collaboration collaboration between the Swiss Institute of Baioinformatics and the EMBL outstation.

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TENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWANH 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aqualysin
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 15-23.

SEQUENCE FROM N.A., AND SEQUENCE OF 15-23.

MEDLINE=90216674; PubMed=2182621;

Terada I., Kwon S.-T., Miyata Y., Matsuzawa H., Ohta T.;

"Unique precursor structure of an extracellular protease, aqualysin I. with NH2- and COOH-terminal pro-sequences and its processing in Escherichia coli.";

J. Biol. Chem. 265:6576-6581(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kwon S.-T., Terada I., Matsuzawa H., Ohta T.,
"Nucleotide sequence of the gene for aqualysin I (a thermophilic
alkaline serine protease) of Thermus aquaticus YT-1 and
characteristics of the deduced primary structure of the enzyme.";
Eur. J. Biochem. 173:491-497(1988).
                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                          SEQUENCE OF 75-442 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-BEPES-2003 (Rel. 41, Last annotation update)
Aqualysin I precursor (EC 3.4.21.-).
                                                                                                                                                                                                                513 AA
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                                                                                                   338 -NRYAYMSGTSMASPHVAGLAALL 360
                                                                          DSKYAYMGGTSMATPIVAGNVAQL 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.-ENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                152 TYTATGRGVNVYVIDTGIRT-----THREFGGRARVGYDALG--GNGQDCNGHGTHVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 NHDSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGAT----DIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 ----VNGAYTIDSRNVDDYVRKNDMAV----LFAAGNEGPNGGTISAPGTAKNAITVGA
                                                                                                                                                                                                                                 (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                              11.6%; Score 260.5; DB 1; Length 513; 28.2%; Pred. No. 1.5e-09; ive 43; Mismatches 157; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
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DDFDFE6D4ASOB785 CRC64);
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STRAIN=168;
MEDLINE=17158234; PubMed=9004506;
Margot P., Karamata D.;
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR009020; Protease Inhib.
Prom; PR00082; Peptidase_S8; I.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE_ASP; I.
PROSITE; PS00136; SUBTILIASE_HIS; I.
PROSITE; PS00137; SUBTILIASE_ERR; I.
HYdrolase; Serine protease; Zymogen; Signal.
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513 AA;
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Bacillus subtilis
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RECENTINE F. Ogasawara N., Moszer I., Braun M., Borchert S.,

RA AZEVEGO V., Bertero M.G., Bessieres P., Brototin A., Borchert S.,

RA AZEVEGO V., Beruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connetroft A., Ehrlich S.D., Emmerson P.T.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Fujita Y., Puma S., Galizzi A., Galleron N.,

RA Fritz C., Fujita M., Fujita N., Fulich S., Galizzi A., Galleron N.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Mallado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mallado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Presecan B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Scolfone P.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

RA Takeuchi M., Tamakar T., Tarkahashi H., Takemaru K.,

RA Takeuchi M., Tamakar T., Tarkahashi H., Takemaru K.,

RA Takeuchi M., Tamakar T., Wanner K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto H., Vannier R., Yasumoto H., Vannier R., Yasumoto H., Wannier R., Yasumoto H., Wannier R., Yasumoto H., Wannier R., Yasumoto H., Yasumoto H., Yasumoto G. the Gram-positive bacterium Bacillus

RA The Complete Genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
he wprA gene of Bacillus subtilis 168, expressed during exponential owth, encodes a cell-wall-associated protease."; crobiology 142:3437-3444(1996).
                                                                                                                      Seror S.J.;
and citG (289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i. FUNCTION: NOT YET KNOWN; COULD BE INVOLVED IN PROTEOGLYCAN DEGRADATION, BY CLEAVAGE OF ITS PEPTIDE BRIDGES.
-i. SUBCELLULAR LOCATION: Cell-wall bound.
-i. PTM: PROCESSED INTO CWBP23 AND CWBP52.
-i. SIMILARITY: Belongs to peptidase family S8.
                                                                                                                    Medina N., Vannier F., Roche B., Autret S., Levine A., "Sequencing of regions downstream of addA (98 degrees) degrees) in Bacillus subtilis."; Microbiology 143:3305-3308(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subtilist; Edilâ46; wprA.
InterPro; IPR000209; Peptidase_S8.
PFEAM; PF00082; Peptidase_S8; 1.
PRO723; SUBTILISIN.
PROSTIE; PS00136; SUBTILIASE_ASP; FALSE_NEG.
PROSTIE; PS00137; SUBTILIASE_HIS; 1.
PROSTIE; PS00137; SUBTILIASE_HIS; 1.
                                                                                                  MEDLINE=98015415; PubMed=9353931;
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HSSP; Q45670; 1DBI.
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                growth,
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138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                767 LGSAKAGKUNAFKVNIATQKQDQVLYLKATKGDAKTSYKVVVVKG-----KPSGTPKVN 820
                                                                                                                                                                                                                                                                                                                                                                                                                   LIAVVDTGVDSTLAD-----LKGKVRTDLGHNFVGRNNNAMDDQGHGTHVAGIIAAQSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 INHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWANHDSKYAYMGGTSMAT
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                                                                                                                                                                                                                                                                                                                                                                             VVAVADTGLDTGRNDSSMHEAFRGKITAIYA---LGRTNNANDPNGHGTHVAGSVLG---
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                          (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                     61; Mismatches 157; Indels 132;
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Betzel C., Klupsch S., Papendorf G., Hastrup S., Branner S.,
Wilson K.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 821 AVKTK--DTAVKGKANSKAMIRVKNKSKKVIASAKADAKGTFSVKIK 865
                                                                                                                                                                                                                                                                                          Length 894;
                                                            WALL-ASSOCIATED PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 NDFTAPYDNNWDGRNN-----VEN-----VFINAPQSGTYTVEVQ
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01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Subtilisin Savinase (BC 3.4.21.62) (Alkaline protease).
Bacillus lentus.
Bacteria, Firmicutes; Bacillales; Bacillaseae; Bacillus.
protease; Cell wall; Zymogen; Signal;
                                                                                                                                                                                                                                                  OF67C353E55F8DBC CRC64;
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L -> I (IN REF. 1)
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MEDLINE=96184541; PubMed=8654411;
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Best Local Simi
Matches 117;
Hydrolase;
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269 AA;
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                                                                              RAY CRYSTALLOGRAPHY (0.78 ANGSTROMS).

RAY CRYSTALLOGRAPHY (0.78 ANGSTROMS).

RAY CRYSTALLOGRAPHY (0.78 ANGSTROMS).

RAY CRUD P., Knapp M., Soltis S.M., Ganshaw G., Thoene M., Bott R.;

RUD P., Knapp M., Soltis S.M., Ganshaw G., Thoene M., Bott R.;

RI Subtilisin.";

Biochemistry 37:13446-13452(1998).

C. - CATALYTIC ACTIVITY: Hydrolysis of proteins and peptide amides.

It catalyzes the hydrolysis of proteins with broad specificity of peptide bonds, and a preference for a large uncharged residue.

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity in Pl. Hydrolyses peptide amides.

C. - CATALYTIC ACTIVITY: Bydrolysis of proteins with broad specificity of the preference for a large uncharged residue.

C. - CATALYTIC ACTIVITY: Bydrolysis of proteins with near second in Pl. Hydrolyses peptide amides.

C. - CATALYTIC ACTIVITY: Bydrolysis of proteins with near second in Pl. Hydrolyses peptide amides.

C. - CATALYTIC ACTIVITY: Becreted.

C. - CATALYTIC ACTIVITY: Becreted.

C. - CATALYTHOLOGY: Secreted.

C. - SUBCELLIGAR LOCATION: Secreted.

C. - SUBCELLIGAR LOCATION: Secreted.

C. - SUBCELLIGAR LOCATION: Secreted.

C. - SUBCELLIGAR LOCATION: Secreted.

C. - Supportation, and many mutations which block sportulation at early stages affect expression levels of subtilisin. However, subtilisin contains and the secreted.

C. - SIMILARITY: Belongs to peptidase family S8.

PDB; ICGV; 10-JAN-01.

PDB; IGCV; 11-NOV-98.

PDB; ILX, 11-NOV-98.

PDB; ILX, 11-NOV-98.

PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.

PDB; PDB; ILX, 11-NOV-97.
  Hilbers C.W., van de Ven F.J.M.; due protease Savinase determined
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CALCIUM 2. (VIA CARBONYL OXYGEN).
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"Backbone dynamics of the 269-residue p
from 15N NMR relaxation measurements";
Eur. J. Biochem. 235:629-640(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                            61
                                                                                                                                                                                                                            11 VOAPBAHNR-GLIGSGVKVAVLDIGIST-----HPDLNIRGGASFVPGEP-STODGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -STYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNHLKNTATSLGSTNL---YGSG
                                                                                                                                                                                                                                                                                                                              62 HGTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 E--NLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 HDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGYPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quax W.J.;
"Cloning, characterization, and multiple chromosomal integration of a Bacillus alkaline protease gene.";
Appl. Environ. Microbiol. 57:901-909(1991).
                                                                                                                                                                       8 VKADVAQSSYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNG
                                                                                                              54; Gaps
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STRAINEPB92,
MEDLINE-91282483; PubMed=2059048;
van der Laan J.C., Gerritse G., Mulleners L.J.M., van der Hoek R.A.,
                                                  Length 269;
                                                  Query Match
11.4%; Score 257; DB 1; Length 26
Best Local Similarity 30.3%; Pred. No. 1.1e-09;
Matches 91; Conservative 38; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCB_TaxID=1445;
26698 MW; 4D89F8778999BF8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELYA BACAO STANDARD; PRT; 380 AA. P27631; Object 1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 10-OCT-2003 (Rel. 24, Last annotation update) Bacillus alcalophilus.
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--STYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNHLKNTATSLGSTNL---YGSG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 HGTHVAGSV--LGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGARI 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 HGTHVAGTIAALNNSIGVLGVAPNAELYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 HINSWGAPVNGAYIIDSRNVDDYVRKNDMAVLFAAGNEGPNGGIISAPGTAKNAIIVGAI
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STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
MEDLINE=93043753; Pubmed=1368952;
Takami H., Kobayashi T., Kobayashi M., Yamamoto M., Nakamura S., Aono R., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acho R., Horikoshi K.; "Molecular cloning, mucleotide sequence, and expression of the structural gene for alkaline serine protease from alkaliphilic Bacillus Sp. 221." Blockem. 56:1455-1460(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.4%; Score 257; DB 1; Length 38 30.3%; Pred. No. 1.7e-09; ive 38; Mismatches 117; Indels
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NCBI_TaxID=79880,
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TD ELYA BACS STANDARD, PRT; 380 AA.

AC 01-1362,
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 42, Last sequence update)
DT 00-COV-2003 (Rel. 42, Last annotation update)
DE 10-COV-2003 (Rel. 42, Last annotation update)
DE 31kaline procease precursor (EC 3.4.21..).
OS Bacillus clausii.
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Best Local Similarity 30.3%;
Matches 91; Conservative
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R INCEPPRO, IPRO002039; Procease_Inhib.

R RICHER, RR00723; SUBTLIASE_S8.

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THAN 130-SCHOOL PROTEASE.

THAN 130-SCHOOL RELAY SYSTEM.

THAN 131 173 173 CALCIUM 1.
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                                                                                                van der Laan J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset O., Mulleners L.J.M., Dijkstra B.W.;
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Martani M., Schipper D., Boelens R.;
"The solution structure of serine protease PB92 from Bacillus alcalophilus presents a rigid fold with a flexible substrate-binding
                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
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-!- COFACTOR: Binds 2 calcium ions per subunit.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to peptidase family S8.
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EMBL; A13738; CAA01128.1; -.
PIR; A49778; A49778.
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186 E--NLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWAN 243
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REDLINE=5536832; PubMed=7632397;

A Kobayashi T., Hakamada Y., Adachi S., Hitomi J., Yoshimatsu T., Kobayashi T., Hakamada Y., Adachi S., Hitomi J., Yoshimatsu T., A Kobayashi T., Hakamada Y., Adachi S., Hitomi J., Yoshimatsu T., A Kobayashi T., Barachi S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., Ito S., I
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
M-protease (EC 3.4.21.-)
Bacillus sp. (Strain KSM-K16).
Bacteria; Firmicutes; Bacillales; Bacillus.
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--- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
--- SUBCELLUTAR LOCATION: Secreted.
--- SIMILARITY: Belongs to peptidase family S8.
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Microorganisms in alkaline evironments, pp.187-194, VCH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVSADANOTNAIWGLDRIDORNLPLDNNYSANFDGTGVTAYVIDTGV-----NNAHVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPVSGLSGSSGQVAYYYVDVEAGQRLTVQMYGGS-------GDADLYLRF--G
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                                                                 calcium-dependent,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                         KASP; 0-9405; 1MrI.

R MEROPS; 080.050; -.

R MEROPS; 080.050; -.

R InterPro; IPR001209; Peptidase_S8.

R InterPro; IPR001209; Procease inhib.

DR Pfam; PF00121; PPC, 1.

DR PRINTS; PR001723; SUBTILASE_ASP; 1.

DR PROSITE; PS00136; SUBTILASE_ASP; 1.

DR PROSITE; PS00137; SUBTILASE_ASP; 1.

DR PROSITE; PS00137; SUBTILASE_ASP; 1.

DR PROSITE; PS00137; SUBTILASE_ASP; 1.

RW Hydrolase; Serine procease; Zymogen; Signal.

FT SIGNAL

22 141 POTENTIAL.

FT ALKLINE EXOP
[1]
SEQUENCE FROM N.A. Mode=2546861; Mode D.R.; Deane S.M., Robb F.T., Robb S.M., Woods D.R.; Noclectide sequence of the Vibrio alginolyticus caldetergent-resistant alkaline serine exoprotease A."; Gene 76:281-288(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%; Score 252.5; DB 1;
larity 26.1%; Pred. No. 5e-09;
Conservative 61; Mismatches 151;
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CHARGE RELAY SYSTEM
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HSSP; Q99405; IMPT.
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Best Local Similarity
Matches 122; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E--NLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSFWAN 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
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Vibrio alginolyticus.
Vibrio alginolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7A03C86D534A1D07 CRC64;
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alkaline serine exoprotease A precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 255; DB 1; 30.4%; Pred. No. 1.4e-09; ive 32; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              268
269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserv
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EMBL; X03341; CAB56500.1;
PIR; A24111; SUBSCL.
PDB; 1AF4; 16-JUN-97.
PDB; 1AV7; 01-APR-98.
         STANDARD;
                                                          SELENOCYSTEINE-325
         SUBT BACLI
P00780;
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InterPro; IPR000209; Peptidase S8.
InterPro; IPR000209; Protease Inhib.
Pfam; PF00082; Peptidase S8; 1.
PRONTS; PR00723; SUBTILISIN.
PROSTE; PS00136; SUBTILISE AP; 1.
PROSTE; PS00136; SUBTILASE AP; 1.
PROSTE; PS00138; SUBTILASE FIRS; 1.
PROSTE; PS00138; SUBTILASE ERR; 1.
PROSTE; PS00138; SUBTILASE ERR; 1.
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31-AUG-94.
31-OCT-93.
18-MAR-98.
15-JAN-95.
25-MAR-98.
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X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 106-379.

MEDLINE=98087517; PubMed=9425066;
Stoll V.S., Eger B.T., Hynes R.C., Martichonok V., Jones J.B.,

Dai E.F.;

Total based protease inhibitors: crystal structures of gamma-
and subtilisin Callsberg complexes.";

Biochemistry 37-451-462(1998).

L. FUNCTION: Subtilisin is an extracellular alkaline serine protease,
it catalyzes the hydrolysis of proteins and peptide amides.

L. FUNCTION: Subtilisin is an extracellular alkaline serine protease,
it catalyzes the hydrolysis of proteins with broad specificity

C. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity

C. CATALYTOR Spride bonds, and a preference for a large uncharged residue
in Pl. Hydrolyzes peptide amides.

C. SUBCELLULAR LOCATION: Secreted.

C. SUBCELLULAR LOCATION: Secreted.

Alcalase by Novozymes

C. MISCELLANEOUS: Secretion of subtilisin is associated with onset of
sportlation, and many mutations which block sportlation at early
is not access of the process of subtilisin is associated with onset of
stages affect expression levels of subtilisin. However, subtilisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Duropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRANT-MCIB 6816;
MEDLINE-6609368; PubMed=3001653;
Jacobs M., Eliasson M., Uhlen M., Flock J.-I.;
"Cloning, sequencing and expression of subtilisin Carlsberg from Bacillus licheniformis.";
Nucleic Acids Res. 13:8913-8926 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECTENCE OF 106-379.

MEDLINE=68234702, PubMed-4967581;
Smith E.L., Delange R.J., Evans W.H., Landon M., Markland F.S.;
Subth E.L., Delange R.J., The complete sequence; comparison with
"Subtilisin Carlsberg. V. The complete sequence; comparison with
subtilisin BPN'; evolutionary relationships.";
J. Biol. Chem. 243:2184-2191(1968).
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Syed R., Wu Z.P., Hogle J.M., Hilvert D.;
"Crystal structure of selenosubtilisin at 2.0-A resolution.";
Biochemistry 32:6157-6164(1993).
            485 AK-----PILNAWDCRPFKYGNNETCTVSATQSGRYHVMIQGYS 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus licheniformis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MUTANT WITH
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                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Subtilisin Carlsberg precursor (EC 3.4.21.62)
                                                                                                                                                                                                       379 AA
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282 GA------VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 ---STYATLNGTSMASPHVAGAAALI------LSKHPNLSASQVRNRLSSTATYLGS 363
                                                                                                                                                                                                            67 GHGTHVAGSV--LGNGTSNKGMAPQANLVFQSVMDSNGGLGGLPSNVSTLFSQAYSAGAR 124
                                                                                                                                                                                                                                    125 IHTNSWGAPVNGAYTIDSRNVDDYVRKNDMAVLFAAGNEGPNG--GTISAPGTAKNAITV 182
                                                                                                                                                                                                                                                                                                                         225 VINMSLGGP---SGSTAMKQAVDNAYARGVVVVAAAGNSGSSGNTNTIGYPAKYDSVIAV 281
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                                                      11.1%; Score 250.5; DB 1; Length 379; 30.2%; Pred. No. 4.3e-09; tive 42; Mismatches 112; Indels 59;
379
38908 MW; F19A6DC5761FB504 CRC64;
                                                        Query Match
Best Local Similarity 30.2%
Matches 92; Conservative
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379 AA;
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Search completed: March 31, 2004, 16:05:32 Job time: 8.51154 secs

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March 31, 2004, 16:09:09; Search time 33.1412 Seconds (without alignments) 3418.697 Million cell updates/sec
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1 NDVARGIVKADVAQNNFGLY......BVQAYNVPVSPQTFSLAIVH 433
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3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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61 NANDPNGHCTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
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                        181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSF
                                                                                                                  241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITFKPSLLKAALIAGAADIGLGY
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TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
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94.4%; Score 2125.5; DB 1
Best Local Similarity 93.5%; Pred. No. 3.3e-178;
Matches. 406; Conservative 19; Mismatches 8;
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APPLICANT: SATO, TSTYOSHI
APPLICANT: SATO, TSTYOSHI
APPLICANT: SATO, TSTYOSHI
APPLICANT: SUNITOMO, NOBUTUKI
APPLICANT: SUNITOMO, NOBUTUKI
APPLICANT: SUNITOMO, NOBUTUKI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KORAYASHI, TOHRU
APPLICANT: KORAYASHI, TOHRU
APPLICANT: KORAYASHI, TOHRU
APPLICANT: KORAYASHI, TOHRU
APPLICANT: KORAYASHI, TOHRU
APPLICANT: NOWURA: ANSAFUMI
FILER ERFERENCE: 234938US
CURRENT APPLICATION NUMBER: US/10/385,662
CURRENT FILING DATE: 2003-03-12
PRIOR FILING DATE: 2002-06-06
PRIOR PELING DATE: 2002-16-18
PRIOR FILING DATE: 2002-10-18
PRIOR FILING DATE: 2002-10-18
NUMBER: OF SEQ ID NOS: 20
SECTRARE: PATENTIN VARBER: JF 2002-304231
SEQ IN NO 2
SECTRARE: PATENTIN VARBER: JF 2002-304231
SEQ IN NO 2
SECTRARE: PATENTIN VARBER: JF 2002-304231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/10385662; Publication No. US20040002432A1; GENERAL INFORMATION:
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US-10-385-662-2
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Best Local Similarity 93.5%; Pred. No. 3.3e-178;
Matches 406; Conservative 19; Mismatches 8; Indels
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APPLICANT: GGAMA, AKINGRI
APPLICANT: GGAMA, AKINGRI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUNTTOWO, NOBUTUKI
APPLICANT: SAEXI, KATSUHISA
TITLE REPRENUE: 215483150
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2000-111-22
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
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301 PNGNQGWGRVTLDKSLNVAYVNESSALSTSQKATYTFTATAGKPLKISLVWSDAPASTTA 360
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Publication No. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: AGGENAM, AKINORI
APPLICANT: SAGENAM, AKINORI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUMITOMO, NGBUYUKI
APPLICANT: SUMITOMO, NGBUYUKI
APPLICANT: SARION NGBUYUKI
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APPLICANT: SARION NGBUYUKI
APPLICANT: SARION NGBER: US/09/985,689A
TITLE OF INVENTION: Alkaline proteases
FILE REFRENCE: 215483USO
CURRENT FILING DATE: 2002-07-01
FRIOR FILING DATE: 2001-04-12
FRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
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ORGANISM: Bacillus sp.
US-09-985-689A-6
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                                                             241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY
                                                                                                                                                                                        301 PNGNQGWGRVTLDKSLNVAYYNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA
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94.1%; Score 2118.5; DB 1

Best Local Similarity 93.3%; Pred. No. 1.3e-177;

Matches 405; Conservative 18; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09985689A
PUBLICATION NO. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: GGAMA, AKINORI
APPLICANT: RAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYCSHI
APPLICANT: SATO, TSUYCSHI
APPLICANT: SATO, TSUYCSHI
APPLICANT: SARKI, HIROYUKI
APPLICANT: SARKI, HIROYUKI
APPLICANT: SARKI, MITSUYOSHI
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SARKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
TILLE OF INVENTION: Alkaline proteases
TILLE OF INVENTION: Alkaline proteases
TILLE OF INVENTION: Alkaline proteases
TILLE OF INVENTION: Alkaline proteases
TILLE OF INVENTION: Alkaline proteases
FILLE REFERENCE: 216483US
CURRENT FILLING DATE: 2000-10-07-01
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATEURING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATEURING VETSION 3.1
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ORGANISM: Bacillus sp.
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US-09-985-689A-2
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88.9%; Pred. No. 1.1e-170;
iive 24; Mismatches 24;
                                                    APPLICANT: GAMA, AUJI
APPLICANT: GAMA, AKINGRI
APPLICANT: GAMA, AKINGRI
APPLICANT: GAMA, AKINGRI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUMITOWO, NOBUYUKI
APPLICANT: SUMITOWO, MISUYOSHI
APPLICANT: SUMITOWO, MISUYOSHI
APPLICANT: STARI, KARISHISA
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: UP P2000-355166
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SEQ TWARE: PATENTIN VERSION 3:1
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Publication No. US20030022351A1
GENERAL INFORMATION:
A PEPLICANT: HATADA, YUJI
A PEPLICANT: OGAWA, AKINORI
A PEPLICANT: SATO, TSUYOSHI
A PEPLICANT: SATO, TSUYOSHI
A PEPLICANT: ARAEXAAM.
US20030022351A1
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Best Local Similarity 88.9%
Matches 385; Conservative
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ORGANISM: Bacillus sp.
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                                                                                                                                                                                        GRUEGES APPLICATION US/09985689A
FUBLICATION NO. US20030022351A1
GRNERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: AGGRVAA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUMITOMO, NOBUYUI
APPLICANT: SUMITOMO, NOBUYUI
APPLICANT: SUMITOMO, NOBUYUI
APPLICANT: SAEKI, KATSUHIGA
ITILE OF INVENTION: ALKAILINE AP
ITILE OF INVENTION: ALKAILINE
FILE REFERENCE: 215483US0
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2001-04-12
NUMBER: OF SEQ ID NOS: 7
SEQ ID NO S: 7
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US-09-985-689A-3
; Sequence 3, Application US/09985689A
PVSPQTFSLAIVH 433
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ORGANISM: Bacillus sp
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; Sequence 13, Application US/10403105
; Publication No. US20030180933A1
; GENERAL INFORMATION:
    APPLICANT: Bauditz, Peter
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
    TITLE OF INVENTION: Protease Variants And Compositions
; TITLE OF INVENTION: Protease US/10/403,105
; CURRENT FILING DATE: 2003-03-31
; PRIOR PILING DATE: 1998-11-19
; PRIOR PILING DATE: 1998-11-19
; PRIOR FILING DATE: 1998-11-19
; PRIOR FILING DATE: 1998-11-19
; PRIOR FILING DATE: BARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 18
; SGOTUMAR: PatsCEC for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 345
; TYPE: RRT

CORGANISM: Bacillus
US-10-403-105-13
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        SEQ ID NO 10
LENGTH: 345
TYPE: PRT
ORGANISM: Bacillus
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| Publication No. US20030176304A1
| GENERAL INFORMATION:
| APPLICANT: Hansen, Peter
| APPLICANT: Bauditz, Peter
| APPLICANT: Mikkelsen, Frank
| APPLICANT: Mikkelsen, Frank
| APPLICANT: Mikkelsen, Frank
| APPLICANT: Mikkelsen, Frank
| TITLE OF INVENTION: Protease Variants and Compositions
| FILE REFERENCE: 5349.204-03
| FILE REFERENCE: 5349.204-03
| FRICK APPLICATION NUMBER: US/09/512,251A
| PRIOR FILING DATE: 2000-02-24
| NUMBER OF SEQ ID NOS: 12
| SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.3%; Score 2033; DB 10;
Best Local Similarity 88.7%; Pred. No. 4.4e-170;
Matches 384; Conservative 25; Mismatches 24;
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: OKUDA, MITSTYOSHI
APPLICANT: SAEKI, KATSUHISA
ITTLE OF INVENTION: ALKALINE proteases
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR RELING DATE: 2000-112
PRIOR RELING DATE: 2000-114048
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2010-04-12
PRIOR FILING DATE: 2010-04-12
PRIOR FILING DATE: 2010-04-12
PRIOR FILING DATE: 2010-04-12
PRIOR FILING DATE: 2010-04-12
PRIOR FILING BATE: 2010-04-12
TYPE: PRI
TYPE: PRI
TYPE: PRI
CRAMISM: Bacillus SP.
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US-10-336-324-10
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APPLICANT: HYARTHA, HIGATH
APPLICANT: HYARTHA, Michael
APPLICANT: MORISHITA, Michael
APPLICANT: MORISHITA, Michael
APPLICANT: SHOWOO, TOWGOO
APPLICANT: KATO, IKUNOSHIN
ITILE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAURALE
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT APPLICATION NUMBER: US/445,472
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-06-10-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 412;
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Publication No. US20020132335A1
GENERAL INFORMATION:
                                                                                                                                                      Sequence 1, Application US/10090624
Publication No. US20020132335A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Pyrococcus furiosus US-10-090-624-1
                        | : ||:||:|
506 GYYNPTAGTWTVKVVSY
402 FINAPOSGTYTVEVQAY
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127; Conservative
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Best Local S:
Matches 127
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                                                                        209 VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW 268
                                                                                                                                                                     269 ANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHGTHVAGSVLG----NATNKGMAPQANLVFQSIM--DSGGGLGGLPANLQTLFSQAYSA 120
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149 GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT 208
                                                                                                                                     241 ANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP 300
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APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASACHA, Kiyozo
APPLICANT: ASACHA, Kiyozo
APPLICANT: ASACHA, Kiyozo
CURRENT APPLICATION NUMBER: US/10/09,624
CURRENT FILING DATE: 2002-03-06
CURRENT FILING DATE: 1999-12-06
PRIOR PRILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 659
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/10090624
Publication No. US20020132335A1
GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
                                                                                                                                                                                                                          301 NGNQGWGRVTLDKSLNV 317
                                                                                                                                                                                                                                                                      329 NGNOGWGRVTLDKSLNV 345
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235 INDYYTAAPGISMATPHVAGIAALLQ-----AHPSWTPDKVKTALIETADIVKPDEI 287
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                                                                                                                                                                                                      70 THVAGSVIG-----NATNKGMAPQANLVFQSIM--DSGGGLGGLPANLQTLFSQAYSAGA 122
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                                                              16 NFGLYGOGOIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNAN-----DPNGHG
                                                                                                              20 NLGYDGSGITIGIIDTGID-----ASHPDLQGKV-----IGWVDFVNGRSYPYDDHGHG
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Gaps
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288 ADIAYGA-----GRVNAYKAINYDNYAKLVFTGYVANKGSQTHQFVISGASFVTATLY 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
APPLICANT: TAKAKURA, Hikaru

APPLICANT: MORISHITA, Mio

APPLICANT: MORISHITA, Mio

APPLICANT: SHIMOJO, TOMOKO

APPLICANT: ASADA, KAYOZO

APPLICANT: KATO, IKUNOShin

TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

FILE REFERENCE: TAKAURA=6

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 09/445,472

PRIOR APPLICATION NUMBER: 151969/1997

PRIOR APPLICATION NUMBER: 151969/1997

PRIOR FILING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 4

LENGTH: 522
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Publication No. US20020132335A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, KYYOZO
APPLICANT: ASADA, KYYOZO
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
17.6%; Score 396; DB 13; Length 5:
Best Local Similarity 29.5%; Pred. No. 5.3e-26;
Matches 127; Conservative 56; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATTON: (428) .. (428)
; OTHER INFORMATION: Xaa at position 428 is Gly or Val.
US-10-090-624-4
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382 TWTIKVVSYS 391
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US-10-090-624-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Query March
17.6%; Score 396; DB 13; Length 6
Best Local Similarity 29.5%; Pred. No. 7.3e-26;
Matches 127; Conservative 56; Mismatches 163; Indels
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Sequence 12251, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHEAA, TADAYOSHI
APPLICANT: SHEAA, TADAYOSHI
APPLICANT: SHEAA, TADAYOSHI
APPLICANT: SHEAD, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANTON NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR PLILNG DATE: 2001-08-02
CURRENT APPLICATION NUMBER: US/10/090,62
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR PEDLICATION NUMBER: 09/445,472
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR PEDLICATION NUMBER: 151969/1997
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 654
                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-10-090-624-16
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226 ILSARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLK 285
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                                                                                                                      Query Match
15.8%; Score 355; DB 14; Length 1208;
Best Local Similarity 31.7%; Pred. No. 7.2e-22;
Matches 126; Conservative 51; Mismatches 151; Indels 70; Gaps
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; SEQ 1D NO 13251

; LENGTH: 1208

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-13251
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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 31, 2004, 15:58:38; Search time 11.3246 Seconds (without alignments) 3677.911 Million cell updates/sec Run on:

US-09-985-689A-7 2252 1 NDVARGIVKADVAQNNFGLY.......EVQAYNVPVSPQTFSLAIVH 433

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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RESULT 1 T18279 multidrug ree C, Species: Di C, Date: 15-0c C, Acession: R, Shoulsky, R, Shoulsky, R, Shoulsky, A, Reference I A, Reference I A, Residues: Dr A, Residues: Dr A, Residues: C, Cosserefe: C, Gonetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics: C, Genetics:	Query M Best Lo Matches	<i>\$</i> ₹3	\ 8 \ 8	දු පු	상 원	\text{5} \frac{1}{2}	& ଶ	S S

304 --- QGWGRVTLDKSLNVAPVNETS----------PLSTS 329 

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Figure 1. Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Kritakani A.; Makasone, 4317-4331, 2000

Aritle: Andrasone, 4317-4331, 2000

Aritle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and Aritle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and Areference: mulber: A83650; MulD:20512582; PMID:11058132

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Arcoss-references: strain C-125

G;Genetics:
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Argoerimental source: strain C-125
              intracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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                                                                                                                                                                                                                                         RESULT 2
T18267
multidrug resistance protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18267
R;Shaulsky, G:; Kuspa, A.; Loomis, W.F.
R;Shaulsky, G:; Kuspa, A.; Loomis, W.F.
R;Shaulsky, G:; Kuspa, A.; Loomis, W.F.
R;Shaulsky, G:; Kuspa, A.; Loomis, W.F.
A;Secretion: T18267
A;Description: An MDR transporter/serine protease gene is required for prestalk speciali
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                                                                                                          --- NWDGRNNVENVFINAPQSGTYTVEVQAYNVPVSPQTFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYGQGQIVAVADTGLDTGR---NDS----SMHEAFRGKITALYALGRTNNANDP--N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHGTHVAGSVLGN-----ATNKGMAPQANLVFQSIMDSGGLGGLPANLQTLFSQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHGTHVCGSAAGTPEDSSWAISSFSGLATDAKIAFYD-LSSGSSEPTPPEDYSQMYKPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAGARIHTNSWGA----PVNGAYTTDSRNVDDYVRK-NDMTILFAAGNEGPGSGTISAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAKNAITVGAEQTAHVNYVSDALEYYDFSDNANFQRPCLFDKKYCNYTTAKCCSEVSNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NHVAQFSSRGPTRDGRIKPDVMAPGTYILSARS
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-----AQAGKPLK---ISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.0%; Score 494.5; DB 2; llarity 28.1%; Pred. No. 8.8e-25; Conservative 72; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAKNAITVGATENLRPSFGS-----YADNI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVTPKPSLLKAALIAGAADVG----
                                                                                                          380 VGNDFTAPYDN-
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Best Local Similarity
Matches 162; Conserv
  QKATYSFT
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intracellular alkaline serine proteinase aprX - Bacillus subtilis
CiSpecies: Bacillus subtilis
CiSpecies: Bacillus subtilis
CiSpecies: Diblo-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
CiAccession: A56587
CiAccession: A56587
CiPace: Osbor-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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CiPace: Osbor-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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CiPace: Osbor-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
CiPace: Osbor-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
CiPace: Osbor-1997 #text_change 15-Oct-1999
CiPace: Osbor-1997 #text_change 15-Oct-1999
Anthors: Fouldar, D.; Entitat, M.; Fulita, M.; Fulitat, W.; Pabret, C.; Ferrari, B.
Anthors: Lauber, J.; Hanaut, A.; Hibert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapiduk, A.; Lardinois Anthors: Lauber, J.; Lararevic, V.; Lee, S.M.; Levine, A.; Lui, H.; Masuda, S.; Mause, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sakaie, Y.; Sato, T.; Scanlon Anthores: Scalidar, A.; Tanaka, T.; Terpeira, P.; Tosato, V.; Ostivan, A.; Tanaka, T.; Terpeira, P.; Tosato, V.; Ostivan, A.; Tanaka, T.; Terpeira, P.; Tosato, V.; Ostivan, A.; Muthors: Voshikawa, H.F; Zumancto, H.; Yanmane, K.; Yasumcto, K.; Yata, K.; Yoshida, A.; Reference number: A69580; MUID:98044033; PMID:9384377
A;Gecssion: A69580; MuiD:98044033; PMID:9384377
A;Gecssion: A69580; MuiDeic acid sequence not shown; translation not shown
                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- EWCIQYNEEHPDDPIHIISMSLGGQALPYENEQEDPMVRIVEEAWNAGITVCVAAGN 292
                                                                                                                                                                                                                                                  EVIRNGETLICKDVILAVIDIGI -----YPHEDLEGRIKAFVDFVNQREEPYDDNGHG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGTYILSARSSLAPDSSF----WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRG 276
                                                                                                                                                                                                                                                                                                                                   THVAGSVLGNATN-----KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAGARI 124
                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 HINSWGAPVNGAYIIDSRNV-------DDYVR-----KNDMIILFAAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGVNIVSLRS---PNSFYDKIQKGSRVGSHYTMMSGTSMATPVCAGVVALMIQH-----
                                                                                                                                                                                                                                                                                                                                                                                             BGPGSGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMA
                                                                                                                                                                      11 DVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALY-ALGRINNANDPNGHG
                                                                                         Gaps
                                                                                     91;
        Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 VTPKPSL----LKAALIAGA---AD-----VGLGF-----PNGNQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
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Query Match
14.9%; Score 334.5; DB 2;
Best Local Similarity 30.5%; Pred. No. 6e-15;
Matches 106; Conservative 50; Mismatches 100;
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175
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Matches
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C.Species Bacillus subtilis
C.Species Bacillus subtilis
C.Dacession: Adilla subtilis
C.Dacession: Adilla subtilis
C.Bacteriol. 17-011-192 #sequence revision 17-011-192 #text_change 20-0un-2000
R.Siloma, A; Ruigo 10 Jr. Glar, Theriault, K.A.; Dwyer, M.; Wilson, S.W.; Pero, J.
J. Bacteriol. 173, 6889-6895, 1391
A; Ristona, A; Ruigo and characterization of the gene for an additional extracellular serine
A; Reference number: Adilla MUDD: 92041574; PMID: 193892
A; Residues: 1-806 < SLD>
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A;Residues: 1-442 <KUN>
A;Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13610.1; PID:e1183385; A;Cross-references: strain 168
C;Genetics:
A;Gene: aprX
C;Superfamily: subtilisin homology
F;146-398/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 VAAGNSGPDSQTIASPGVSEKVITVGALDDNNTA----SSDDDTVASFSSRGPTVYGKEK 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 PDILAPGVNIISLRS---PNSYIDKLQKSSRVGSQYFTMSGTSMATPICAGIAALILQ-- 399
                                                                                                                                                                                                                                                                                                                                                                                PNGHGTHVAGSVLGNATN-----KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GAYTIDSRNVDDYVRKND-----MIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 FAAGNEGPGSGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 PDVMAPGTYILSARSSLAPDSSF----WANHDSKYAYMGGTSMATPIVAGNVAQLREHF 271
                                                                                                                                                                                                                                                                                                                                   EVVRNGQTLTGKGVTVAVVDTGI-----YPHPDLEGRI----IGFADMVNQKTEPYD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IEGVEWCIQYNEDNPDEPIDIMSMSLGGDALRYDHEQEDPLVRAVEEAWSAGIVVC 288
                                                                                                                                                                                                                                                                                                                                                                                                               DVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNAN-
                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                          66
                                                                                                                                                                                            DB 2;
                                                                                                                                                                                       14.1%; Score 316.5; DB 2 30.9%; Pred. No. 9.5e-14;
                                                                                                                                                                                                                                          41; Mismatches
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                                                                                                                                                                                                                                          104; Conservative
                                                                                                                                                                                                                Similarity
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Best Local S
Matches 104
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A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Voshidaw, H.F.; Zumatein, B.; Yoshidawa, H.; Danchin, A.; Aritle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A65580; MUID:98044033; PMID:9384377
A; Reference number: A65580; MUID:98044033; PMID:9384377
A; Rocession: D69730
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-806 ckUN>
A; Residues: 1-806 ckUN>
A; Cross-references: GB:299123; GB:AL009126; NID:92636240; PIDN:CAB15835.1; PID:92636344
A; Experimental source: strain 168
C; Comment: The amino terminal sequence of the mature protein and a molecular weight of C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDG--RNNVENVF 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKDLIGKVAVVKRGSIAFVDKADNAKKAGAIGMVVYNNLSGEIEANVPGMSVPTIKLSLE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DPRGEATDHGTHVAGTVAANGTIKGVAPDATLLAYRVLGPGG--SGTTENVIAGV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194
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SREAISVGATQLPLNEYAVTFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKDFE 396
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T28159
Pyrolysin (EC 3.4.-.-) - Pyrococcus furiosus
Dyrolysin (EC 9.4.-.-) - Pyrococcus furiosus
C;Species: Pyrococcus furiosus
C;Species: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 24-Oct-2000
C;Accession: T28159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLAPDSSFWANHDSKYAYMGGISMAIPIVAGNVAQLREHFVKNRGVIPKPSL--LKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 IAGAADV----GLGFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 MNTAVTLKDSDGEVYPHNAQGAG-----SARIMNAIKADSLVSPGSYSY----GTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---FILENOSS-IRKSYTLEYSFNGSGISTSGTSRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NDSSMHEAFRGKITALYALGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERAVODGADVMNLSLGNSLNNPDWATSTAL-DWAMSEGVVAVTSNGNSGPNGWTVGSPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | : | | | : | | | : DLGYJGKGIKVAIIDJGVEYNHPDLKKNFGQYKGYDFVDNDYDPKBTPTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , DB 2; Le
6.8e-13;
ches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 NFGLYGOGQIVAVADTGLDTGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 309;
llarity 23.2%; Pred. No. 6
Conservative 58; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPAHOTGKATAKVKVNTKKTKAGTYEGTVI
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nes 132, Conserv
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63

189;

799;

Length

12.6%; Score 283.5; DB 2; llarity 24.5%; Pred. No. 3.4e-11; Conservative 48; Mismatches 127;

homology

200

228 512 288 561 343

--VAQFSSRGPT-RDGRIKPDVMAPGTYILS

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:|||| | ; | : | ::| SVGAT---RLPYNKYKASVFTSDGIDYPSADIMGFPSDEELLELDGETYEYAFAGLGKPG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 DFEGVDVEGKIALIVRGBIPFVEKAENAKAAGAVGAIIYNNVAGVQPTVPGLAIPTIMLS 452
                                                                                                                                                                                                                                                                                                                                             453 NEDGLKMRNELENGQNTVTFSIEFDKLVGETVADFSSRGPVMHTWMIKPDVSAPGVAIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 MNTAENLVDENGNRYPHNTQGAG-----SIRIVDAIESETLVTPGSHSFGTFTKERGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPNG----HGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGR-----TINN-----AN
C;Superfamily: microbial serine proteinase vpr; subtilisin
C;Reywords: hydrolase; serine proteinase
F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                           Query Match
Best Local Similarity
Matches 118; Conserv
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           C.; Siezen, R.J.; Vos,
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       R;Voorhorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, J. Biol. Chem. 271, 20462-20431, 1996
A;Title: Isolation and characterization of the hyperthermostable serine prote A;Title: Isolation and characterization of the hyperthermostable serine prote A;Reference number: 220481; MUID:96355370; PMID:8702780
A;Reference number: 220481; MUID:96355370; PMID:8702780
A;Status: T2884
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 11398
A;Orose-references: EMBL:US5835; NID:g1556462; PID:g1556463; PIDN:AAB09761.1
A;Experimental source: DSM3638
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.1%;
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IAGAADV----GLGFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATY-SFTAQAGKP

LK 345

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Serine proteinase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris pv. c. N;Alternate names: subtilisin-related proteinase c. Species xanthomonas campestris pv. campestris c.;Species xanthomonas campestris pv. campestris c.;Date: 21-Nov-1993 #sequence_revision 07-Feb-1997 #text_change 03-Dec-1999 C;Accession: S11890 R;Liu, Y. N.; Tang, V.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J. No.; Tang, V.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J. No.; Daniels, M.J. No.; Tang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.L.; Prang, V.
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llarity 27.8%; Pred. No. 4.1e-11;
Conservative 49; Mismatches 152;
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us-09-985-689a-7.rpr

1	RESULT 10 S23407 subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39) C;Species: Bacillus sp. C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999 C;Date: 05-Davai, S2407 R;Narinx, B.; Davai, S.; Feller, G.; Gerday, C. Bjochim. Biophys. Acta 1131, 111-113, 1992 A;Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarcti A;Reference number: S23407; MUID:92256481; PMID:1581352 A;Residues type: DARA A;Residues: 1-420 <ara 1-420="" <ara="" a;cross-references:="" a;residues:="" embl:x62369;="" nid:g40200;="" pid:g40201<="" pidn:caa44227.1;="" th=""><th>C;Genetics: A;Gene: subl C;Gene: subl C;Superfamily: subtilisin; subtilisin homology C;Superfamily: subtilisin; subtilisin homology C;Superfamil: subtilisin; protein; hydrolase; serine proteinase F;1-23/Domain: signal sequence #starus predicted <frg> F;12-420/Product: microbial serine proteinase #status predicted <mat> F;136-374/Domain: subtilisin homology <sbt> F;136-374/Domain: subtilisin homology <sbt> F;145,185,360/Active site: Asp, His, Ser #status predicted Query Match 11.8*; Score 566; DB 1; Length 420; Bast Local Similarity 31.4*; Pred. No. 2.18-10; Matches 97; Conservative 40; Mismatches 114; Indels 58; Gaps 17;</sbt></sbt></mat></frg></th><th>  CLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGT</th><th>Qy 128 SWGAPVNGAYTIDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGATENL 187                                       </th><th>QY 242 NHDSKYAYMGGTSMATPIVAGNYAQLREHFVKNRGVTPKPSLLKAALIAGAA 293  bb 349 -FDGGYATISGTSMASPHAAGLAAKIWAQYPSASNVDVRGELQYRAYENDILSGYYAGYG 407  QY 294 DVGLGF 299  bb 408 DDFASGFGF 416</th><th>RESULT 11 S25835 subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41) C;Species: Bacillus sp.</th></ara>	C;Genetics: A;Gene: subl C;Gene: subl C;Superfamily: subtilisin; subtilisin homology C;Superfamily: subtilisin; subtilisin homology C;Superfamil: subtilisin; protein; hydrolase; serine proteinase F;1-23/Domain: signal sequence #starus predicted <frg> F;12-420/Product: microbial serine proteinase #status predicted <mat> F;136-374/Domain: subtilisin homology <sbt> F;136-374/Domain: subtilisin homology <sbt> F;145,185,360/Active site: Asp, His, Ser #status predicted Query Match 11.8*; Score 566; DB 1; Length 420; Bast Local Similarity 31.4*; Pred. No. 2.18-10; Matches 97; Conservative 40; Mismatches 114; Indels 58; Gaps 17;</sbt></sbt></mat></frg>	CLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGT	Qy 128 SWGAPVNGAYTIDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGATENL 187	QY 242 NHDSKYAYMGGTSMATPIVAGNYAQLREHFVKNRGVTPKPSLLKAALIAGAA 293  bb 349 -FDGGYATISGTSMASPHAAGLAAKIWAQYPSASNVDVRGELQYRAYENDILSGYYAGYG 407  QY 294 DVGLGF 299  bb 408 DDFASGFGF 416	RESULT 11 S25835 subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41) C;Species: Bacillus sp.
HTSHADLNANILAGYDFISDATTARDGNGRI HYAGSVLGNATNKGMAPQANLV HYAGGYGAAVTHTTGVAGTAYGAKVVPVRU QTLESQAYSAGARIHTNSWGAPVNGAPVNGATT ANPAEVINMSLGGGGSCSTTMQNA-INGAVSI FIISAPGTAKNALITVGATENLRPSFGSYAI TISAPGTAKNALITVGATENLRPSFGSYAI	Db 378DVSAPGSSILSTINSGTTTPGSSYASYNGTSMASPHVAGVVALVQS 424  Qy 272 VKNRGVTPKPSLLKAALIACAADVGLGF	RESULT 9 T29030 Surface layer-associated STABLE proteinase - Staphylothermus marinus NiAlternate names: hyperthermostable proteinase CiSpcies: Staphylothermus marinus CiSpcies: Staphylothermus marinus CiSpcies: Staphylothermus marinus CiSpcies: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 CiAccession: T29030 CiAccession: T29030 CiAccession: T3993 Curr. Biol. 6, 733-749, 1996 A;Title: A hyperthermostable protease of the subtilisin family bound to the surface laye A;Title: A hyperthermostable protease of the Subtilisin family bound to the surface laye A;Reference number: Z20559; WUID:96385442; PMID:8793300	A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: Last contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains a	Query Match       12.3%; Score 277.5; DB 2; Length 1345;         Best Local Similarity 27.3%; Pred. No. 1.7e-10;         Matches 124; Conservative 66; Mismatches 157; Indels 107; Gaps 23;         Qy       46 FRGKITALYALGRINNANDPNGHGTHVAGSVLGNATNKGWAPQANLV 92         Db       445 YQGRYLALVSDFHGHGTSVATVIASRGRVLYDLYGDGKLYRIMGVAPGAKI- 495	QY         93 FQSIMDSGGGLPANLQTLFSQAYSAG	QY 177 NAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPQTYILSARS 231

predicted <CTP>

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F;497-715/Domain: carboxyl-terminal propeptide #status predic
F;239-294,335-372,478-481/Disulfide bonds: #status predicted
                                                                                             Query Match
Best Local Similarity 25.3%;
Matches 118; Conservative 5
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A;Map position: 1
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R/TSujibo, H.; Miyamoto, K.; Tanaka, K.; Kaidzu, Y.; Imada, C.; Okami, Y.; Inamori, Y.
Biosci. Biotechnol. Blotchem. 60, 1284-1288, 1996

A/Title: Cloning and sequence analysis of a protease-encoding gene from the marine bacte
A/Title: Cloning and sequence analysis of a protease-encoding gene from the marine bacte
A/Reference number: JC4908, MUID:97141200, PMID:8987544

A/Reference number: JC4908, MUID:97141200, PMID:898754

A/Residues: 1-715 <-75U-
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A/Cross-references: DDBJ:D38600, MID:91536787, PIDN:BAA18912.1; PID:d1019647, PID:g21602
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C;Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999 C;Accession: S25835
R;Davail, S.; Feller, G; Narinx, E.; Gerday, C.
Grin 119, 143-144, 1992
A;Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotraction to mumber: S25835, MUID: 93012966; PMID:1398082
A;Accession: S25835
A;Molecule type: DNA
A;Accession: S25835, MUID: 93012966; PMID:1398082
A;Molecule type: DNA
A;Cross-references: EMBL:X63533; NID:940198; PIDN:CAA45096.1; PID:g40199
C;Superfamily: subtilisin, subtilisin homology
C;Superfamily: subtilisin, subtilisin hydrolase; serine proteinase
F;1-23/Domain: signal sequence #status predicted <BCO
F;1-23/Domain: signal sequence #status predicted <BCO
F;111-1419/Product: microbial serine proteinase #status predicted <AMI>F;135-373/Domain: subtilisin homology <BED:
F;144,184,359/Active site: Asp, His, Ser #status predicted
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Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
             22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GQGQIVAVADTGLDTGRNDSSMH-EAFRGKITALYALGRT---NNANDPNGHGTHVAGSV
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    Alteromonas

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Best Local Similarity 30.9
Matches 95, Conservative
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serine proteinase, subtilase family - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: D75393
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.; Shen, M.; Vener, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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A;Nolecule type: DNA
A;Residues: 1-627 <WHI>
A;Cross-references: GB:AE001990; GB:AE000513; NID:g6459214; PIDN:AAF11026.1; PID:g64592
A;Experimental source: strain Rl
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                                                                                                                                                                                                                                                                                                                      242 DSSGQPVPRADQDSSWHGTHVAGTVAAVTNNGEGVAGVAYDAKVVPVRVL---GKCGGLT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 NEGPGSGTISAPGTAKNAITVGAT--ENLRPSFGSYADNINHVAOFSSRGPTRDGRIKPD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 VAAPG----GAQSFADDPEGILSTHNSGSGAPSNDSYHYSQGTSMAAPHVAGVAALIKQ- 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 N-ETSPLSTSQKATYSFTAQAGKPLKISLVWSDAP-GSTTASLTL----VNDLDLVI---T 372
                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                   -NGHGTHVAGSVLGNATN----KGMAPQANLVFQSIMDSGGGLGGLP 107
                                                                                                                                                                                                                                                                                                                                                                                                     ANLOTLFSQAYSAGARIHTNSWGAPV-----NGAYTTDSRNVDDYVRKNDMTILFAAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AKPSATPDEVETILKNTTRSFAGSC-----SNCGTGVVDAAAAVNEALG 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYGOGOIVAVADTGLDTGRNDSSMHEAFRGKITALYALGR-----TNNANDPNGHGTHV
                                                                                                                                                                                        GGGVVVAVLDIGYRPHLDLDANILPGYDMISNTFVANDGGARDNDARDPGDAVTRGECGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDIADGIIWASGGSDRVPANANPAVVINMSLGGGGACSATTONAINOARNNGTVIVIAAG
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                                                                                                                                 21 GQGQIVAVADTG----LDTGRNDSSMHEAFRGKITALYALGRTNNANDP---
Length
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11.6%; Score 261.5; DB 2;
Best Local Similarity 28.0%; Pred. No. 7.3e-10;
Matches 92; Conservative 49; Mismatches 122;
11.7%; Score 262.5; DB 2; 25.3%; Pred. No. 7.4e-10; iive 51; Mismatches 176;
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Qy 128 SWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGFGSGTISAPGTAKNAITVGATENL 187	Db 509 AKKLVDQEGVPHEIHEQGAGRIQVDKAVATSLVYPGALSFGK 551
ML-KAGVVPVFAIGNFGPAG	Qy 348 LVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNW 392
188 RPSFGSYADNINHVAQFSSRGPTR-DGRIKPDVMAPGTYILSARSSLAPDSSFWA 24	DD 552WSKDDLREKRPVTLTIENH-DTVKRTYHISPPFDVPDGVEW 591
326	RESULT 15
QY 242 NHDSKYAYMGGTSMATPIVAGNVAQLREHFVKORGVTPKPSLLKAALIAGAADVGL 297 :	APE0607 - Aeropyrum pe
OY 298 GFPNGNQGMGRVTLDKSLNVAFVNETSP 325  Dh 418 KNNNVGFGOTGTPGALGKT.GVGFTP 443	C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 C;Accession: A72647 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa. H. Takamiva. M.: Masuda. S.: Punahashi, T.; Tanaka, T.; Yandoh, Y.; Yamazaki, J.;
	per-thermophilic Crenarchaeon, A
RESULI 14 C84121 subtilisin-type proteinase (EC 3.4.21) BH3763 precursor [similarity] - Bacillus halodu	A;Reteriore number: A/2#30; Null:99910339; FMID:10302500 A;Scatus: preliminary
C,Species: Bacillus halodurans C,Date: 0.1 Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C.bression: 784730	A;Molecule type: DNA A;Rosidues: 1-131 cKAW- A.Crost-references: DDB1:AP000060: NID:G5104188: PIDN:BAA79577.1; PID:d1043363; PID:G51
, N.; Fuji, F.;	
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and   A;Reference number: A83650; MUID:20512582; PMID:11058132	
A;Accession: C84120 A;Status: preliminary A;Molecule type: DNA	Query Match 11.5%; Score 258; DB 2; Length 1331; Best Local Similarity 23.8%; Pred. No. 3.5e-09; Matches 107; Conservative 65; Mismatches 149; Indels 128; Gaps 19;
A,Residues: 1-757 <sto> A,Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07482.1; GSPDB:GN0d A,Experimental source: strain C-125</sto>	55
C, Genetics:	Db 360 ALSDIGMISGRPDPSILDLSFADETPASYGSEVLARDFIGDGVNDFSAGALAGWTYDWVG 419
Ajuene: Dazios C.Superfamily: microbial serine proteinase vpr; subtilisin homology C;Keywords: hydrolase; serine proteinase F;1-20/Domain: signal sequence #status predicted <sig></sig>	Qy 56LGRTNNAN
Query Match 11.5%; Score 258; DB 2; Length 757;	Qy 83KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAG 121
Best Local Similarity 22.6%; Pred. No. 1.68-09; Matches 119; Conservative 56; Mismatches 156; Indels 196; Gaps 20;	Db 479 GYIETSLRGVAPGAKIAAGGSFLINVFVAQLFLSGFEPQDSPLNWVYTG 527
QY 8 VKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALG 57	Qy 122ARIHTNSWQAPVNGAYTTDSRNVDDY-VRKNDMTILFAAGNEGFGSGTISAP 172 :
QY 58 RINNANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQA 117	QY 173 GTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSAR 230
118 YSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGGGTISAPGTAKN 1.	
DD SES VEDGEDVILLEDEGNI VNGFENFIGEREDEGNA CEGG VAN I "ONGNOGENGAL VGGGGGON ZOO"  178 DITHYDRI	
288 AISVGASAPPLNTPYLTAFGEENEISLYPFSGGLPWAFKRDLPMIDVGYGTEKEWEGVDA 3	704 TARDTGADAFTQGSGQVDVYRAVK-AVLEGGVPIALSTSVYENVYSLLSGYSYPFLA
Qy 194 200	Qy 341 GKPLKISLVWSDAPGSTTASLTLVNDL 367
Db 348 EGKVVLIKRGMVPFTEKVMHAVAAKARGVIIYNNTPGPFTGMIEGGVNIPVVSITREDGE 407	Db 760 PNPVEDTQIYPGVLKPGETAVETLVLKTL 788
Qy 201	Search completed: March 31, 2004, 16:10:23 Job time : 12.3246 Becs
234 APDSSFWANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAG 2	
464 IPNNGYLGINGTSMAAPHVAGAAALIKQAHPEWTPEQVKAALMNT 5	
CY 292 AADVGLGFPNGNQGWGRVTLDKSLNVAFVNETSFLSTSQKATYSFTAQAGKFLKIS 347	

bacillus su bacillus li bacillus pu thermoactin schizosacch

bacteroides caenorhabdi

bacteroides trichoderma

tritirachiu

P58502 P04189 P00781 P07518 P04072 P20015 P20015 P22781 P42781 P42779

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
SIMILARITY: In the N-terminal section; belongs to peptidase family
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PROSITE; PS50229; ABC_TRANSPORTER_1; 1.
PROSITE; PS50201; ABC_TRANSPORTER_2; 1.
PROSITE; PS50301; ABC_TRANSPORTER_2; 1.
PROSITE; PS50136; SUBTILASE_ASP; FALSE_NEG.
PROSITE; PS00131; SUBTILASE_HIS; 1.
PROSITE; PS001318; SUBTILASE_HIS; 1.
PROSITE; PS001318; SUBTILASE_SESP; FALSE_NEG.
Hydrolase; Serine protease; ATP-binding; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
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Shaulsky G., Escalante R., Loomis W.F.;
"Developmental signal transduction pathways uncovered by genetic
                                                                                                                                                                                                                                                                                                                                                                                CLNOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagC precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                 ALIGNMENTS
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PIR, T18279; T18279.
DictyBase; DDB0001095; tagC.
InterPro; IPR0001569; AAA, ATP866.
InterPro; IPR00140; ABC_TM transpt.
InterPro; IPR003439; ABC_transptr.
InterPro; IPR003499; PBC transptr.
Pfam; PP00664; ABC_membrane, 1.
Pfam; PP00065; ABC_tran; 1.
Pfam; PP00085; PEDTidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
SUBIT BACST
TKSU PYRKO
SUBIT BACSU
SUBIT BACSU
UBIT BACPU
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                                    715 SLVQGWGAIRMSNWLHVVNNNNSNNNNKTSDGITKFDGIGGLDLRLVKPNQWKEESLSTG 774
                                                     QKATYSFT-----AQAGKPLK---ISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKY 379
655 VDGYYPTGSIVESNKLQPTGSLLKALMINNAQLLNGTFQLITSSSITYPSNQVFENFAGA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes Dev. 9:1111-1122(1995).
--- FUNCTION: Intercellular communication via tagB may mediate integration of cellular differentiation with morphogenesis.
--- SIMILARITY: In the N-terminal section; belongs to peptidase family
                                                                                                        S8.
--- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
--- SIMILARITY: STRONG, TO TAGC.
                                                                  380 VGNDFTAPYDN------NWDGRNNVENVFINAPQSGTYTVEVQAYNVPVSPQTFS
                                                                                                                                                                                                                                                                          STRAIN=AX4;

MEDLINE=55262903; PubMed=7744252;

Shaultsky G., Kuspa A., Loomis W.F.;

"A multidrug resistance transporter/serine protease gene is required

for prestalk specialization in Dictyostelium.";

Genes Dev. 9:1111-1122(1995).
                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prestalk-specific protein tagB precursor (EC 3.4.21.-).
                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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ive 79; Mismatches 165; Indels 194; Gaps
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotini A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotini A., Borchert S.,

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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Brow S.,

RA Borriss R., Codani J.J., Connetron I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Connetron I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,

RA Diniseppi G., Guy B.J., Haga K., Haiech J., Gallarai A., Gallaron N.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hibert W., Koetter P., Komingstein G., Krogh S., Kumano M.,

RA None D., O'Reilly M., Dawada S., Mauel C., Medigue C.,

RA Mone D., O'Reilly M., Ogawa R., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Senor S., Reperon P., Schleich S., Schroere R., Schfone F.,

RA Sato T., Scanlan E., Schleich S., Schror P., Shin B.S., Soldo B.,

RA Rieger M., Taconi B., Takagi T., Takahari H., Takemaru K.,

RA Scoxkin A., Taconi B., Takagi T., Takahari H., Takemaru K.,

RA Rewchi M., Tamakoshi A., Taranka T., Terpstra P., Tognoni A.,

RA Pakeuchi M., Tamakoshi A., Taranka T., Terpstra P., Tognoni A.,

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RA Pakeuchi M., Wandutt R., Wedler E., Wedler F., Weitzenegger T.,

RA Viari A., Wandutt R., Wedler E., Wedler F., Weitzenegger T.,
344 -LKISLVMSDAPGSTTASLTLVNDLDL-----VITAPN--GTKYVGNDFTAPYDNN 391
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Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Dancohin A.,
"Bacillus subtilis genome project: cloning and sequencing of the
kb region from 325 degrees to 333 degrees.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Minor extracallular procease vpr precursor (EC 3.4.21.-).
VPR OR IPA-45R OR BSU38090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                      392 WDGRNNVENVFINAPQSGTYTVEVQAYNVPVSPQTFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                903 -DTLNNVEGIIINPTKAMNYKFTIAGTNVPIGPQKFS 938
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MEDLINE=92041574; PubMed=1938892;
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Pyrococcus furiosus.
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Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.",
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(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).
                                                                                                              Nature 390:249-256(1997).
-!- FUNCTION: NOT REQUIRED FOR GROWTH OR SPORULATION.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PIM: PROBABLY UNDERGOES C-TERMINAL PROCESSING OR PROTEOLYSIS.
-!- PIM: PROBABLY UNDERGOES C-TERMINAL PROCESSING OR PROTEOLYSIS.
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Interbro; IPR003137; PA.

Interbro; IPR003137; PA.

Interbro; IPR009020; Peptidase S8.

Interbro; IPR009020; Protease_inhib.

Pfam; PF002025; PA; 1.

PRINTS; PR001021; PEPTILISIN.

PROSITE; PS001136; SUBTILIASE ASP; 1.

PROSITE; PS00137; SUBTILIASE ASP; 1.

PROSITE; PS00137; SUBTILIASE ASP; 1.

PROSITE; PS00138; SUBTILIASE ASP; 1.

PROSITE; PS00138; SUBTILIASE ASP; 1.

PROSITE; PS00138; SUBTILIASE ASP; 1.

PROSITE; PS00138; SUBTILIASE ASP; 1.

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PROSITE; PS00138; SUBTILIASE ASP; 1.

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EMBL; X73124; CAA51601.1; -.
EMBL; Z99123; CAB15835.1; -.
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HSSP, P00782; 2SBT.
MEROPS; S08.UPA; -.
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STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=6635370; PubMed=8702780;
Voorinorst W.G.B., Eggen R.I.L., Geerling A.C.M., Platteeuw C., Siezen R.J., de Vos W.M.;
Siezen R.J., de Vos W.M.;
Tisolation and characterization of the hyperthermostable serine protects, pyrolysim, and its gene from the hyperthermophilic archaeon Pyrococcus furiosus.";
                                                                                          564 MNTAVTLKDSDGEVYPHNAQGAG-----SARIMMAIKADSLVSPGSYSY----GTFL
                                                 289 IAGAADV----GLGFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPL
517 PTHDPD------AKPKWSVEQISMASPHIAGAVAVIKQ------AKPKWSVEQIKAAI
                                                                                                                                                          KISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDG--RNNVENVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-YOI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-00T-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-00T-2003 (Rel. 42, Last annotation update)
Pyrolysin precursor (BC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1398 AA
                                                                                                                                                                                                                                                                      INAPOSGTYTVEVQAYNVPVSPQTFSLAIV 432
                                                                                                                                                                                                                                                                                                                  Biol. Chem. 271:20426-20431(1996).
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EMBL, AE010153, AAL80411.1, -
PIR, T28159, T28159.
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STRAINSACTOR 33931, NGPPB 528;

RATANSACTOR 33931, NGPPB 528;

RATANSACTOR 33931, NGPPB 528;

RATANSACTOR 33931, NGPPB 528;

RATE SIVEN A.C.R., Ferror J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RATOURD C. C. Canavan F., Cardoxo J., Clambergo F., Clapina L.P.,

RATOURD C. C. Canavan R.D., Courinho L.L., Clambergo F., Clapina L.P.,

RATOURD F. Ferreira A.J.S., Ferreira R.C., Gruber A.,

RATSUYAMA A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RATSUYAMA A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RATSUYAMA A.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souca R.F.,

RA Spinola L.A.F., Takita M.A., Tandfil D., Teai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.; Takita M.A., Tandra S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.; Takita M.A., Tandra S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.; Takita M.A., Tandra S.M., White R.F.,

RA Setubal J.C., Sitajima J.P.; Low Xanthomonas pathogens with differing RT host specificities S.M.,

RA Setubal J.C., Sitajima J.P.; Leite R.B., Milly S8.

RA SINILARITY: Belongs to peptidase family S8.
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                                SKYAYMGGISMAIPIVAGNVAQLREHFVKNRGVIPKPSLLKAALIAGAA-----DVGLG 298
                                                                    FPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTT
                                                                                                                                            MEDLINE=90251253; PubMed=2187155;
Liu Y.-N., Tang J.-L., Clarke B.R., Dow J.M., Daniels M.J.;
"A multipurpose broad host range cloning vector and its use to
characterise an extracellular protease gene of Xanthomonas campestris
                                                                                               YTELDOGHGLVNVTKSWEI------LAMINGTTLPIVDHWADKSYSDF
                                                                                                                         359 ASLTLVNDLDLVITAPNG-----TKYVGND-----FTAPYDNNWDG-----RNN
                                                                                                                                                                                                                                                                                                                                                                              Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                VENVE----INAPQSGTY-----TVEVQAYNVPVSPQTFS 428
                                                                                                                                                                                                  TEFVLRVKYDVEGLEPGLYVGRIIIDDPTTPVIEDEILNTIVIPEKFT 788
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PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Complete proteome.
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InterPro; IPR000209; Peptidase_SB.
InterPro; IPR007280; PPC.
Pfam; PF00082; Peptidase_SB; 1.
Pfam; PF04151; PPC; 1.
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| GSGTVVAVIDTGITSHADLNANILAGYDFISDATTARDGNGRDSNAADEGDWYAANECGA
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                                    GQGQIVAVADTGL----DTGRNDSSMHEAFRGKITALYALGRTNNAND
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%; Score 279.5; DB 1; 27.8%; Pred. No. 4.6e-11; iive 49; Mismatches 152;
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01-DEC-1992 (Rel. 24, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Subtilisin precursor (EC 3.4.21.62).
EMBL; AE012184; AAM40166.1;
PIR, S11890; S11890.
HSSP; PO0782; ZSBT.
MEROPS; S08.UPA, -.
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MEDIINE-92256481; PubMed=1581352;

MEDIINE-92256481; PubMed=1581352;

Marinx E., Davail S., Feller G., Gerday C.;

Muclectide and derived amino acid sequence of the subtilisin from
AT "Nuclectide and derived amino acid sequence of the subtilisin from
The antarctic psychrotroph Bacillus TA39.";

Biochim. Biophys. Acta 1131:111-113(1992).";

Eliochim. Biophys. Acta 1131:111-113(1992).";

Eliochim. Biophys. Acta 1131:111-113(1992).";

C. I. CATALVITC ACTIVITY: Hydrolysis of proteins and peptide amides.

C. CATALVITC ACTIVITY: Hydrolysis of proteins with broad specificity
for peptide bonds, and a preference for a large uncharged residue
C. I. COPACTOR: Binds I calcium ion per subunit (Potential).

C. SUBCELLANEOUS: Scilla active at temperatures close to 0 degrees
C. I. MISCELLANEOUS: Scilla active at temperatures close to 0 degrees
C. MISCELLANEOUS: Scilla active at temperatures close to 0 degrees
C. MISCELLANEOUS: Scilla active at temperatures close to 0 degrees
C. MISCELLANEOUS: Scilla active at temperatures close to 0 degrees
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C. MISCELLANEOUS: Scilla active at temperatures close to 0 degrees
C. MISCELLANEOUS: Scilla active at temperatures close to 0 degrees
C. MISCELLANEOUS: Scilla active at temperatures close to 0 degrees
C. Subculation, and many mutations which block sporulation at early stages affect expression levels of subtilisin. However, subtilisin is not necessary for normal sporulation.
C. SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQGQIVAVADTGLDTGRNDSSMHEAFRGKITAL--YALGRT---NNANDPNGHGTHVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 VL----GNATNKGMAPQANL-VFQSIMDSGGLG-GLPANLQTLFSQAYSAGARIHTN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 SWGAPVNGAYTIDSRNVDDYVRKNDMIILFAAGNEGPGSGTISAPGTAKNAITVGATENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 RPSFGSYADNINHVAQFSSRGPT-RDG----RIKPDVMAPGTYILSARSSLAPDSSFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zymogen; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 266; DB 1; Length 42 31.4%; Pred. No. 2.3e-10; ive 40; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
SUBTILISIN.
CHARGE RELAY SYSTEM (BY SIM CHARGE RELAY SYSTEM (BY SIM CHARGE RELAY SYSTEM (BY SIM CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
M; AE4F121BD32B26EC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR000209; Peptidase_S8.
Pfam, PF00082; Peptidase_S8; 1.
PRNINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00137; SUBTILIASE_HIS; 1.
PROSITE; PS00139; SUBTILIASE_ERF; 1.
Hydrolase; Sporulation; Serine protes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X62369; CAA4427.1; -. PIR; S23407; S23407. HSSP, Q99405; IMPT. MEROPS; S08.UPA; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calcium-binding, Signal
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Best Local Similarity
Matches 97; Conserv
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324

368 478

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           104 GGLPANLOTLFSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVR----KNDMTILFAAG 160
                                                                                                                                                                                                                                340 VFAPGSQIKSA------W--YDGGYKTISGTSMATPHVAG-VAAL--YLQENSSVS 384
                                          NSNADACNYS-PARVATGVTVGSTTSTDARSFSNWGSCV-----D
                                                                                                                                                                                                                                                                                                       NEGPGSGTISAPGTAKNAITVGAT - - ENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPD
                                                                                                                                                                                    VMAPGTYILSARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVT
                                                                                                                                                                                                                                                                        279 PKPSILKAALIAGAADVGLGFPNGNQGWGRVTLDK-SLNVAFVNETS------
                                                                                                                                                                                                                                                                                                                                                               -----PL----STSQKATYSFTAQAGKPLKISLVWSDAPGSTTASLTLVNDLD
                                                                                                                                                                                                                                                                                                                                                                                                         431 PDPEGKLTSGVPVSGLSGSSGQVAYYYVDVEAGQRLTVQMY----GGS------GDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVITAPNGTKYVGNDFTAPYDNNWDGR-----NNVENVFINAPQSGTYTVEVQAYN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from a
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thermophilic serine proteinase precursor (EC 3.4.21.-) (Ak.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus sp. (strain AKI).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95085262; PubMed=7993087; Macaiver B., McHale R.H., Saul D.J., Bergquist P.L., Cloning and sequencing of a serine proteinse genethermophilic Bacillus species and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.80 ANGSTROMS) OF 122-401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appl. Environ. Microbiol. 60:3981-3988(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR00209; Peptidase S8.
InterPro; IPR009020; Protease Inhib.
Pfam; PF00082; Peptidase S8; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L29506; AAA63688.1; -.
PIR; I39974; I39974.
PDB; 1DBI; 18-NOV-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S08.009; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACSP
                                                                                                  161
                                                                                                                                          300
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NHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSL-----LKAALIAGAA 293
                                          -FDGGYATISGISMASPHAAGLAAKIWAQYPSASNVDVRGELQYRAYENDILSGYYAGYG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 RGKITALY-ALGRINNANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIM--DSGGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IVKADVAQNN--FGL-------YGQGQIVAVADTGLDTGRNDSSMHEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-89326126; PubMed=2546861;
MedlinE-89326126; F.T., Robb S.M., Woods D.R.;
"Nucleotide sequence of the Vibrio alginolyticus calcium-dependent, detergent-resistant alkaline serine exoprotease A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALKALINE SERINE EXOPROTEASE A.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAX SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
84E96D9C649D4226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150;
                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. NCBI_TaxID=663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 254; DB 1; Length 534 26.1%; Pred. No. 1.9e-09; ive 63; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alkaline serine exoprotease A precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 76:281-288(1989).
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zymogen; Signal. POTENTIAL.
                                                                                                                                                                                                                                                 534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 19
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PRO0723, SUBTILLSIN,
PROSITE, PS00136, SUBTILLSE ASP, 1.
PROSITE, PS00137, SUBTILLASE ASP, 1.
PROSITE, PS00138, SUBTILASE SER, 1.
Hydrolase, Serine protease, Zymoger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55930 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 26.1
Matches 124; Conservative
                                                                                                                                                                                                                                              STANDARD;
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180
213
                                                                                                                              DDFASGFGF 416
                                                                                      D---VGLGF 299
                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio alginolyticus
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213
363
363
534 AA,
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MEROPS; S08.050; -.
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Best Local Similarity
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  242
                                            349
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ACT_SITE
SEQUENCE
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P16588;
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66 --NGHGTHVAG---SVLGNATN-KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
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-I. FUNCTION: Subtilisin is an extracellular alkaline serine protease, it catalyzes the hydrolysis of proteins and peptide anides.

-I. CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity for peptide bonds, and a preference for a large uncharged residue in P1. Hydrolyzes peptide amides.

-I. COPACTOR: Binds 2 calcium ions per subunit.

-I. SUBCELLULAR LOCATION: Secreted.

-I. BICTECHNOLOGY: Used as a detergent protease. Sold under the name Savinase by Novozymes.

-I. MISCELLANEOUS: Secretion of subtilisin is associated with onset of sporulation, and many mutations which block sporulation at early
                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 ONNFGLY-----GOGGIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNANDP-
                                                                                                                                                                                                                                                                                                                                                                         137 QNTYIDYAWDVIKGSSGQEIAVIDIGVD-----YTHPDLDGKVIKGYDF--VDNDYDPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMILLFAAGNEGPGSGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 SGAEVINLSLGC---DCHTTTLENAVNYAWNKGSVVVAAAGNN--GSSTTFEPASYENVI
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trystal Structure of the alkaline proteinase Savinase from Bacillus lentus at 1.4-A resolution."; Mol. Biol. 223:427-445(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR.
MEDLINE=96184541; PubMed=8654411;
MEDLINE=96184541; PubMed=8654411;
Remerowski M.L., Pepermans H.A.M., Hilbers C.W., van de Ven F.J.M.;
"Backbone dynamics of the 269-residue protease Savinase determined from 15N-NMR relaxation measurements.";
Eur. J. Biochem. 235:629-640(1996).
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MEDLINE=98426039; PubMed=9753430;
MCDLINE=98426039; Soltis S.M., Ganshaw G., Thoene M., Bott
"The 0.78-A structure of a serine protease: Bacillus lentus
subtilisin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92148829; PubMed=1738156;
Betzel C., Klupsch S., Papendorf G., Hastrup S., Branner S.,
Wilson K.S.;
                                                                                                                                                                                                                                       Length 401;
                                                                                                                                                                                                                                                                                    96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Subtilisin Savinase (EC 3.4.21.62) (Alkaline protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus lentus.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1467;
                                                                                                                                                                                               42835 MW; 1C736EF4A89F256F CRC64;
                                                                                                                                                                                                                                          11.1%; Score 249; DB 1;
31.7%; Pred. No. 2.8e-09;
iive 29; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
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401 AA;
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P29600;
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EMBL, 527501, 527501, 527501.

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                                                                                                                                                                                                                                                                                                                                                                         125 HTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 E--NLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 DQNNNRASFSQYGAGL-----DIVAPGWNVQSTYPG----
                                                                                                                                                                                                          10.9%; Score 245.5; DB 1; Length 269; 31.0%; Pred. No. 2.8e-09; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 HDSKYAYMGGTSMATPIVAGNVA------QLREHFVKN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --STYASLNGTSMATPHVAGAALVKOKNPSWSNVOIRNH-LKN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
Kato C., Nakano Y., Yamamoto M., Horikoshi K.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Intracellular alkaline protease (EC 3.4.21.-).
Bacteria, Firmicutes, Bacillales; Bacillaceae, Bacillus.
NCBI_TAXID=79880;
                      259
261
267
269
2698 MW; 4D89F8778999BF8D CRC64;
                                                                                                                                                                                                                                          Local Similarity 31.09
nes 88; Conservative
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269 AA;
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P29140;
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EMBL; M65086; AAA22212.1; -. EMBL; A13738; CAA01128.1; -. PIR; A49778; A49778. PDB; LAH2; 15-APR-98.
                            Structure 5:521-532(1997)
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                                                                                                                                                                                                158 -----TDSEELHDAVKYAVSNNVSVVCAAGNEGDGREDINEFAYPAAYNEVIAVGAVDFD 212
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                                                                                                                                                                                                                                                                                                                    TNK---GMAPQANLVFQSIM--DSGGGLGGLPANLQTLFSQAYSAG--ARIHTNSWGAPV 133
                                                                                                                                       80
                                                                            40 GAGQIIGVIDIGCQVDHPDLAERIIGGVNLTIDYG-GVETNFSDNNGHGTHVAGTVAAAE 98
                                                                                                                                                                                                                                                      247 YAYMGGTSMATPIVAGNVAQL----REHFVKNRGVTPKFSLLKAALIAGAADVGLGFPNG
                                                          GQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAGSVLGNA
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MEDLINE=91283483; PubMed=2059048;
van der Laan J.C., Gerritse G., Mulleners L.J.M., van der Hoek R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "cloning, characterization, and multiple chromosomal integration of Bacillus alkaline protease gene.", Appl. Environ. Microbiol. 57:901-909(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92290330; PubMed=1518788; van der Laan J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset C Mulleners L.J.W., Dijkstra B.W.; "Crystal structure the high-alkaline serine protease PB92 from Bacillus alcalophilus."
                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin J.R., Milder F.A., Karini-Nejad Y., van der Zwan J.,
Mariani M., Schipper D., Boelens R.;
"The solution structure of serine protease PB92 from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
MEDLINE=391078250; PubMed=144775;
Sobek H., Hecht H.-J., Aehle W., Schomburg D.,
X-ray structure determination and comparison of two crystal
a variant (RanliSArg) of the alkaline procease from Bacillus
alcalophilus refined at 1.85-A resolution.";
J. Mol. Biol. 228:108-117(1992).
   Length 321;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alkaline protease precursor (EC 3.4.21.-).
Bacillus alcalophilus.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
10.9%; Score 245.5; DB 1; 30.4%; Pred. No. 3.5e-09; ive 40; Mismatches 114;
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InterPro; IPR000209; Protease Inhib.
InterPro; IPR000209; Protease Inhib.
InterPro; IPR000209; Protease S8; I.
PROSTE; PR00139; SUBTILASE ASP; I.
PROSITE; PS00138; SUBTILASE HIS; I.
PROSITE; PS00138; SUBTILASE ESR; I.
Hydrolase; Serine protease; Zymogen; Metal-binding; Calcium-binding; Signal; 3D-structure.
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alcalophilus presents a rigid fold with a flexible substrate-binding
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                                                                                                                                               Structure 5:21-532(1997).
1- COFACTOR: Binds 2 calcium ions per subunit.
1- SUBCELLUIAR LOCATION: Secreted.
1- SIMILARITY: Belongs to peptidase family 58.
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                                                                                                                                                                                                                    8 VKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNG
                                                                                                                                                                                                                                                                         122 VQAPAAHNR-GLIGSGVKVAVLDIGIST-----HPDLNIRGGASFVPGEP-STQDGNG
                                                                                                                                                                                                                                                                                                                                            HGTHVAGSV -- LGNATN-KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAGARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 HTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 ANLSLGSPSPSATLEQAVN---SATSRGVLVVAASGNSGAGS--ISYPARYANAMAVGAT
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi K.;
(In) Horikoshi K. (eds.);
Microorganisms in alkaline evironments, pp.187-194, VCH,
Microorganisms in alkaline evironments, pp.187-194, VCH,
Weinheim (1991).
-!- COPACTOR: Binds 2 calcium ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning, nucleotide sequence, and expression of the structural gene for alkaline serine protease from alkaliphilic Bacillus sp. 221.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STEAD ALGORNESS / DSM 2512;
STRAIN=21 / ATCC 21522 / JCM 9139 / DSM 2512;
MEDLINE=93043753; PubMed=1368952;
Takami H., Kobayashi T., Kobayashi M., Yamamoto M., Nakamura Aono R., Horikoshi K.;
                                                                                             Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 HDSKYAYMGGTSMATPIVAGNVA------QLREHFVKN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --STYASLNGTSMATPHVAGAAALVKOKNPSWSNVQIRNH-LKN 357
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=79880;
380
38853 MW; 539EA72771B6682C CRC64;
                                                                                      10.9%; Score 245.5; DB 1;
llarity 31.0%; Pred. No. 4.4e-09;
Conservative 32; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iosci. Biotechnol. Biochem. 56:1455-1460(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 112-129.
STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update
Alkaline protease precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 AA
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D13157; BAA02442.1; -.
A25817; CAA01836.1; -.
A225817; CAA01611.1; -.
F29600; IGCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                 380 AA;
                                                                                                                       Local Similarity
es 88; Conserv
375
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HELIX
SEQUENCE
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                                                                                      Query Match
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EMBL;
HSSP;
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DR InterPro; DV0:1103; -..

InterPro; IPR00020; Protease S8.

InterPro; IPR000320; Protease S8. Inhib.

BR InterPro; IPR000320; Protease S8. I.

BR PROSITE; PR00132; SUBTILASE ASP; I.

BROSITE; PS00133; SUBTILASE ASP; I.

RROSITE; PS00133; SUBTILASE BRR; I.

RHYdrolase; Serine protease; Zymogen; Metal-binding; Calcium-binding;

W Hydrolase; Serine protease; Zymogen; Metal-binding; Calcium-binding;

T SIGNAL I 27 POTENTIAL.

T CHAIN I 380 ALKALINE PROTEASE.

T CHAIN I 380 CHARGE RELAY SYSTEM (BY SIMILARITY).

T ACT SITE 143 173 CHARGE RELAY SYSTEM (BY SIMILARITY).

T ACT SITE 32 26 CHARGE RELAY SYSTEM (BY SIMILARITY).

T METAL 113 113 CALCIUM I (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 HGTHVAGSV--LGNATN-KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAGARI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 VKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 VOAPAAHNR-GLIGSGVKVAVLDÍGIST-----HPDLNIRGGASFVPGEP-STQDGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 HINSWGAPVNGAYTIDSRNVDDYVRKONDMILLFAAGNEGPGSGTISAPGTAKNAITVGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 DONNNRASFSQYGAGL--------DIVAPGVNVQSTYPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Deinococcus-Thermus, Deinococci; Thermales, Thermaceae,
                                                                                                                                                                                                                                                                                                                                                            CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALCIUM 2 (VIA CARBONYL OXYGEN)
(BY SINILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --STYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNH-LKN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 HDSKYAYMGGTSMATPIVAGNVA------QLREHFVKN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 245.5; DB 1; 31.0%; Pred. No. 4.4e-09; ive 32; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Aqualysin I precursor (EC 3.4.21.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA; 38826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.0%;
Matches 88; Conservative 3
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151
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229

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294 PARVAEALTVGATTSSDARASFSNYGSCV---------DLFAPGASIPSA 334
                                                                                                                                                                                                                              230 RSSLAPDSSFWANHDSKYAYMGGTSWATPIVAGNVAQLREHFVKNRGVTP---KPSLLKA 286
                                                                                                                                                                                                                                                                                                                                                                                              --LLSSGSGSTAPCTSCSYYTGSLSGPGDYNF---QPNGTYYYSPAGTHRAWLRGPAGTD 456
                               NDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMD--SGGGLGGLPANLQTLFSQAYSA 120
                                                                                                                             243 -TRNHRRPAVANMSLGGGVSTA-----LDNAVKNSIAAGVVYAVAAGNDNANACNYS- 293
                                                                                                                                                                                                                                                            ------wytsdtatotlngtsmatphvag-vaal--yleonpsatpasvasailng 381
140 IDQRDLPLSNSYTYTATGRGVNVYVIDTGIRT-----THREFGGRARVGYDALG--GNG
                                                 121 GARIHTN-----SWGAPVNGAYTTDSRNVDDYVRKN----DMTILFAAGNEGPGSGTISA
                                                                                                                                                              PGTAKNAITVGAT--ENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSA
                                                                                                                                                                                                                                                                                             287 ALIAGAADVGLGFPNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKI
                                                                                                                                                                                                                                                                                                                                                             SLVWSDAPGST-----TASLTLVNDLDLVITAPNGTKY-------VGND
                                                                                                                                                                                                                                                                                                                                  382 ATTGRLSGIGSGSPN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S08.010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRTM_BACSP
099405;
                                 63
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PRTM BACSP
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                                                                                                                                                                                                                                                                                                                                                                                              The optimal temperature for its caseinolytic activity is 80 degrees Celsius.

The optimal temperature for its caseinolytic activity is 80 degrees Celsius.

-!- SUBCELULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: Secreted from the early stationary phase until the time the cells cease to grow.
-!- PTW: THE N- AND C-TERMINAL PRO-SEQUENCES ARE REMOVED THROUGH THE PROTEOLYTIC ACTIVITY OF AQUALYSIN I ITSELF, IN THAT ORDER. THE C-TERMINAL PRO-SEQUENCES ARE REMOVED THROUGH THE PROTEASES ACROSS THE OWNER MEMBRANE.
-!- PTM: Two disulidade bonds are present.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%; Score 245.5; DB 1; Length 513; 26.0%; Pred. No. 6.5e-09; ive 43; Mismatches 145; Indels 157; Gaps
                   MEDLINE=90216674; PubMed=2182621; Terada I., Ohta T.; Terada I., Kwon S.-T., Miyata Y., Matsuzawa H., Ohta T.; Un'ique precursor structure of an extracellular protease, aqualysin I, with NH2- and COOH-terminal pro-sequences and its processing in Escherichia coli.";
                                                                                                                                                                                                                                                                                               MEDLINE-88151377; PubMed=3162211;
Matsuzawa H., Tokugawa K., Hamaoki M., Mizoguchi M., Taguchi H.,
Matsuzawa H., Tokugawa K., Hamaoki M., Mizoguchi M., Taguchi H.,
Terada I., Kwon S.-T., Ohta T.;
"Purification and characterization of aqualysin I (a thermophilic alkaline serine protease) produced by Thermus aquaticus YT-1.";
Bur. J. Biochem. 171:441-447(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                STRAIN=TI;

MEDLINE=88225062; PubMed=3286255;

Kwon S.-T. Terada I., Matsuzawa H., Ohta T.;

Kwon Serie sequence of the gene for aqualysin I (a thermophilic alkaline serine protease) of Thermus aquaticus YT-1 and characteristics of the deduced primary structure of the enzyme.";

Eur. J. Blochem. 173:491-497(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDFDFE6D4A50B785 CRC64;
                                                                                                                                  SEQUENCE OF 75-442 FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro IPR000209, Peptidase_88.
InterPro IPR009209, Protease Inhib.
Promo Procost Peptidase_88, 1.
PRNNTS, PR00723, SUBTILISIN.
PROSITE, PS00136; SUBTILIASE_ASP; 1.
PROSITE, PS00134; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_RIS; 1.
Hyddrolase; Serine protease; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQUALYSIN I.
                                                                                                    J. Biol. Chem. 265:6576-6581(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90108; BAA14135.1; -. EMBL; X07734; CAA30559.1; -.
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Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A35742; A35742.
HSSP; P06873; 2PRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 :
513 AA;
                                                                                                                                                                                                                                                                                   SEQUENCE OF 128-170
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ACT_SITE
SEQUENCE
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PROPEP
CHAIN
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383

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346 401

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SEQUENCE OF 1-23, AND CHARACTERIZATION.
MEDLINE=9338832; PubMed=7632397;
KObayashi T., Hakamada Y., Adachi S., Hitomi J., Yoshimatsu T.,
Kobayashi T., Hakamada Y., Adachi S., Hitomi J., Yoshimatsu T.,
Koike K., Kawai S., Ito S.,
"Purification and properties of an alkaline protease from
alkalophilic Bacillus Sp. KSM-Ki6.";
Appl. Microbiol. Biotechnol. 43:473-481(1995).
-!- COFACTOR: Binds 2 calcium ions per subunit.
-!- SIMILARITY: Belongs to peptidase family S8.
PDB; 1MPT; 22-JUN-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease; Metal-binding; Calcium-binding;
384 FTAPYDNNWDGRN------NVENVFINAPOSGTYTVEVQAYN 419
                                               457 PDL-YLWRWDGSRWLTVGSSTGPTSEESLSYSGTAGYYLWRIYAYS 501
                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).

Yamane T., Kani T., Hatanaka T., Suzuki A., Ashida T.,

Kobayashi T., Ito S., Yamashita O.;

"Structure of a new alkaline serine protease (M-protease)

Bacillus sp. KSM-K16.';

Acta Crystallogr. D 51:199-206(1995).
                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
M-proctease (EC 3.4.21.-).
Bacillus sp. (strain KSM-K16).
Bacteria, Firmicutes; Bacillales; Bacillus.
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SYSTEM.
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CHARGE RELAY S
CHARGE RELAY S
                                                                                                                                                                                    269
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Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
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3D-structure.
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RA Kunst F., Oggaswara N., Mosser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Broizot F., Deviner K.M., Dusterhoft A., Erhiloh S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kodayashi Y., Koetter P., Koningstein G., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Rudel C., Medique C.,
RA Medina N., Mallado R.P., Mizuon M., Mosetl D., Nakai S., Noback M.,
RA Medina N., Mallado R.P., Mizuon M., Mosetl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Setiguchi J., Sekowaka A., Schroeter R., Scotfone F.,
Schlan E., Schleich S., Schroeter R., Scotfone F.,
Schlan E., Schleich S., Vandench M., Vannier F., Vassarott A.,
RA Takeuchi M., Takayashi H., Weitzenegger T.,
RA Takeuchi M., Tanaka H., Tarkanashi H., Waitzenegger T.,
RA Takeuchi M., Tanaka H., Sator S.J., Serror P., Shin B.S.,
RA Tosato V., Uchlyama S., Vandelor E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Weihiam H., Danchin A.,
RA The complete genome sequence of the Gram-positive bacterium Bacillus
T. "The Complete Genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                        WPRA_BACSU STANDARD; PRT; 894 AA.
P5443; 006726;
01-0071-996 (Rel. 34, Created)
115-DEC-1998 (Rel. 37, Last sequence update)
116-DCT-2003 (Rel. 42, Last annotation update)
Cell wall-associated procease precursor (BC 3.4.21.-) [Contains: Cell wall-associated polypeptides CWBP23 and CWBP52].
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Margot P., Karamata D.;
"The wprA gene of Bacillus subtilis 168, expressed during exponential "The encodes a cell-wall-associated protease.";
Microbiology 142:3437-3444(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168;
MEDLINE=98015415; PubMed=9353931;
Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
Medina N., Vannier P. Roche B., Autret S., Levine A., Seror S.J.;
Megrencing of regions downstream of adda (98 degrees) and citG (289
degrees) in Bacillus subtilis.';
Microbiology 143:3305-3308(1997).
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-! - SUBCELLULAR LOCATION: Cell-wall bound.
-! - PTM: PROCESSED INTO CWBP23 AND CWBP52.
                              206 --STYASLNGTSMATPHVAGVAALVKQKNPSWSNVQIRNH-LKN 246
                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97158234; PubMed=9004506;
243 HDSKYAYMGGISMATPIVAGNVA-
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                                                                                                                                                                                   HGTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHV 119
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ilarity 31.0%; Pred. No. 3.2e-09;
Conservative 32; Mismatches 99;
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268
269 AA;
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 NRMDMTADFSNYGKGL----DISAPGSDI----PSLVPNGN-----VTYMSGTSM 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 ATPYAAAAAGLL---FAQNPKLKRTEVEDMLKKT----ADDISFESVDGGEEELYDDYGD 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TAQAGK--PLKISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N----KGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSAGARIHTNSWGAPVNGAY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 TIDSRNVDDYVRK--NDMILLFAAGNEGPGSGTISAPGTAKNAITVGATENLRPSFGSYA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 DNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWANHDSKYAYMGGTSM 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 ATPIVAGNVAQLREHFVKNRGV--TPKRSLLKAALIAGAADVGLGFPNGNQ------ 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           765 KKLGSAKAGKDNAFKVNIA------TOKODOVLYLKATKG-
                                                                                                                                                                                                                                              Subtlist, BGI1846; wprA.
InterPro; IPR000209; Peptidase_S8.
FRINDS: PR00021 Peptidase_S8.
FRINTS: PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILISE_ASP; FALSE_NEG.
PROSITE; PS00137; SUBTILIASE_ASP; FALSE_NEG.
PROSITE; PS00138; SUBTILIASE_HIS; 1.
Hydrolase; Serine protease; Cell wall; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V -> A (IN REF. 1).
L -> I (IN REF. 1).
OF67C353E55F8DBC CRC64;
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llarity 23.8%; Pred. No. 1.8e-08;
Conservative 68; Mismatches 150;
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-!- SIMILARITY: Belongs to peptidase family S8.
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POTENTIAL.
CWBP52.
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894 AA;
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Matches 110; Conserv
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94.4%; Score 2125.5; DB 2; Length 640;
Best Local Similarity 93.5%; Pred. No. 3.3e-116;
Matches 406; Conservative 19; Mismatches 8; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-EXPA3;
Lich S., Saeki K.;
lich S., Saeki K.;
lich w protease.";
submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO51423; BAB55674.2; - ABO51423; CONOGA289; F:BUBLiase activity; IEA.
GO; GO: 00006508; P:Proteolysis and peptidolysis; IEA.
R Interpro; IPR000209; Peptidase_S8.
R Interpro; IPR00020; Peptidase_S8; I.
R Pfam; PF00082; Peptidase_S8; I.
R Pfam; PF00151; PFC; I.
R RPINTS; PR00173; SUBTILASE_HIS; I.
R PROSITE; PS00137; SUBTILASE_HIS; I.
R PROSITE; PS00137; SUBTILASE_SER; I.
SEQUENCE 640 AA; 67991 MW; 4BBAF77E9D592C15 CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=109322;
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Last annotation update)
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Q82I39
Q9RL54
Q8KKH6
Q9L0A0
Q8GGT4
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      SEQUENCE FROM N.A.
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360 SLTLVNDLDLVITAPNGTKYYGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
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SEQUENCE B
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        AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 179
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=133781;
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GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0004289; F:ubtidase activity; IEA.

GO; GO:0005508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002209; Peptidase_S8.

Pfam; PF0082; Peptidase_S8, 1.

Pfam; PF0082; Peptidase_S8, 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
protease (Fragment).
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PROSTITE; PRO0137; SUBTILASE HIS; 1.
PROSTITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Protease; Serine protease.
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SEQUENCE 434 AA; 45294 MM; 83517E
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                                                                                                                                                                                                                                                                                                                                                                                                                                A MEDLINE-20568675; PubMed=11118284;
A Sacki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H., Sacki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H., Horikoshi K.,
A Horikoshi K.,
Horikoshi K.,
Horikoshi K.,
Horikoshi K.,
Horikoshi K.,
Horikoshi K.,

alkaliphilic Bacillus ssp.: enzymatic properties, sequences, and alkaliphilic Bacillus ssp.: enzymatic properties, sequences, and blochem. Biophys. Res. Commun. 279:313-319(2000).

B Biochem. Biophys. Res. Commun. 279:313-319(2000).

R BABL; ABG46403; BAB21266.2; -.

R BASP; POO782; 1SUP
R GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

R GO; GO:0004289; F:subtilase activity; IEA.

R GO; GO:0004289; F:subtilase activity; IEA.

R GO; GO:0004289; F:subtilase activity; IEA.

R PFOMITS; PRO0723; SUBTILISIN.
R PROSITE; PSO0133; SUBTILISIN.
R PROSITE; PSO0134; SUBTILISEN.
R PROSITE; PSO0138; SUBTILIASE ERR; 1.
SR PROSITE; PSO0138; SUBTILIASE ERR; 1.
SR EQUENCE 639 AA, 68185 MM; 316AF6FPDBE4FF54 CRC64;
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                                                                                                                                                                                                   Bacillus sp. 9860.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=133778;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                  121 GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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                                                                      1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                            61 NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA
                                                                                                                                                                  181 VGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
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  Gaps
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Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami
Horikoshi K.;
  23; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=127889;
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Last annotation update)
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24; Mismatches
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
Protease (Fragment)
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     386; Conservative
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     Matches
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                                                                                                                                                                                                                                           TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF 239
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     NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 265
                                                                                                                                                                                                                                                                       AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGT1SAPGTAKNAI
                                                    NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                 NANDTNGHGTHVAGSVLGNGATNKGMAPQANLVFQSIMDSSGGLGGLPSNLQTLFSQAFS
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"Novel oxidatively stable subtilisin-like serine proteases from alkaliphilic Bacillus ssp.: enzymatic properties, sequences, and evolutionary relationships.";
Biochem. Blophys. Res. Commun. 279:313-319 (2000).
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
EMBL; AR0464605; BAB21268.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=SD521;
MEDLINE=20568675; PubMed=11118284;
Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Horikoshi K.;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=133780,
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GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006289; P:subtilase activity; IEA.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR0007280; PPC.
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Last annotation update)
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PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
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Pfam; PF04151; PPC; 1.
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity
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SEQUENCE
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181 VGATENLRPSFGSYADNINHVAQFSSRGPIRDGRIKPDVWAPGTYILSARSSLAPDSSFW 240
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A Anjard C., Loomis W.F.;

A Anjard C., Loomis W.F.;

Anjard C., Loomis W.F.;

Tevolution of the ABC transporters of Dictyostelium.";

Tevolution of the ABC transporters of Dictyostelium.";

Submitted (JAN-202) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

REMBL; AF466309; AAL174253.1; -..

RGO; GO:00062524; F:ATP binding; IEA.

RGO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...;

RGO; GO:0006233; F:peptidase activity; IEA.

RGO; GO:00065809; F:subtilase activity; IEA.

RGO; GO:00065109; P:proceolysis and peptidolysis; IEA.

RGO; GO:0006810; P:transport; IEA.

RICHEPRO; IPRO01140; ABC_TM_transpt.
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                                                                                                                              90.3%; Score 2033; DB 2; Length 433; 88.7%; Pred. No. 5e-111; 1ve 25; Mismatches 24; Indels
                                                                                        45587 MW; B81291A803C775AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Serine procease/ABC transporter TagD.
PROSITE; PS00138; SUBTILASE_SER; 1.
Hydrolase; Protease; Serine protease.
NON TER 1 1
NON TER 433 433
SEQÜENCE 433 AA; 45587 MW; B81291
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                                                                                                                                 Query Match
Best Local Similarity 88.7%
Matches 384; Conservative
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                                                                                                                                                                                                                                                                                                                    121 GARIHTNSWGAPVNGAYTIDSRNVDDYVRKNDMIILFAAGNEGFGSGTISAPGTAKNAIT 180
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                                                                                                                                                                  1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60
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                                                                                                                                        1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV
                                                                                             Gaps
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Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
Horikoshi K.,
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                                             Query Match
90.6%; Score 2040; DB 2; Length 433;
Best Local Similarity 88.9%; Pred. No. 2e-111;
Matches 385; Conservative 24; Mismatches 24; Indels
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Bacillus sp. Y.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
    AA; 45636 MW; 52087E0A2516107F CRC64;
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Last annotation update)
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PROSITE; PS00137; SUBTILASE HIS; 1.
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Pfam; PF04151; PPC; 1.
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
Protease (Fragment).
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       433
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       SEQUENCE
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Q9AQR2
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Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
NCBI_TaxID=44689;
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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 LREH-----FVKORGVTPKPSLLKAALIAGAADVGLGFP----------------300
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                                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                           ANLQTLFSQAYSAGARIHTNSWGA----PVNGAYTTDSRNVDDYVRKN-DMTILFAAGNE 162
                                                                                                                                                                                                                                                                                                                                                                          -----GSYAD-----NINHVAOFSSRGPTRDGRIKP 217
                                                                                                                                                                                                                                                                                                                                                                                                                 DVMAPGTYILSARSSLA------PDSSFWANHDSKYAYMGGTSMATPIVAGNVAQ 266
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                                                                                                                                                                                                                                                                                                                                GPGSGTISAPGTAKNAITVGATENLRPSF----------------191
                                                                                                                                                                                                                                                                                                                                                   eqyssils-qataknvitvgaeqtthesyttdaleysnfetvakstinsicqsfddkyct 551
                                                                                                                                                                                                      11 DVAQNN----FGLYGQGQIVAVADTGLDTGR---NDS-----SMHEAFRGKITALYAL
                                                                                                                                                                                                                                               57 GRINNANDPNGHGTHVAGSVLGN-----AINKGMAPQANLVFQSI-MDSGGGLGGLP
                                                                                                                                                                                 208;
                                                                                                                                                            Length 1825;
                                                                                                                                                                                155; Indels
                                                                                                                                        E28160BC78613A3B CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                           22.2%; Score 501; DB 5; 27.9%; Pred. No. 1.1e-20; ive 73; Mismatches 155.
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  InterPro; IPR003439; ABC_transporter.
InterPro; IPR00209; Peptidase_S8.
Pfam; PF000664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Pfam; PF00082; Peptidase_S8; 1.
PRNYS; PR00722; SUBTILISTN.
PRODON; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; PROSITE; PS002137; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
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                                                                                                                               Protease; Transport.
825 AA; 202641 MW;
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(TrEMBLrel. 16, 1
(TrEMBLrel. 25, 1
                                                                                                                                                                                   169; Conservative
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                                                                                                                                         1825 AA;
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01-MAR-2001
01-OCT-2003
                                                                                                                              ATP-binding;
SEQUENCE 18
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Matches
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AND SEQUENCE FROM N.A.

RA GOOD J.R., Cabral M., Kuspa A.;

RA GOOD J.R., Cabral M., Kuspa A.;

RI "Taga, a putative serine protease/ABC transporter of Dictyostelium
RT that is expressed at the onset of development and is required for the
RT that is expressed at the onset of development and is required for the
RT that is expressed at the onset of development and is required for the
RT differentiation of a subpopulation of prespore cells.";

RU differentiation of a subpopulation of prespore cells.";

RE SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

BRBL, AP26345; AAGTH16.1; -.

BR GO, GO:0006504; F.ATP binding IEA.

GO; GO:0006509; F.ATP-binding cassete (ABC) transporter acti. . .; IEA
GO; GO:0006109; F.ATP-binding lieA.

GO; GO:0006109; F.ATP-binding lieA.

GO; GO:0006109; F.ATP-binding lieA.

GO; GO:0006109; F.ATP-binding lieA.

BR GO; GO:00061149; ABC TM transpt.

BR InterPro; IPR0013439; AAA ATPASSE.

BR InterPro; IPR0013439; ABC TRANSPORTER.;

BR Ffam; PR000006; ABC TRANSPORTER.;

BR PROSITE; PS00031; ABC TRANSPORTER.;

BR PROSITE; PS00311; ABC TRANSPORTER.;

BR PROSITE; PS00311; ABC TRANSPORTER.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATENLRPSFGSYADNINH-------
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23;

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123 RIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 ATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADIAYGA------GRVNAYKAINYDNYAKLVFTGYVANKGSQTHQFVISGASFVTATLY 472
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420 SWGPPSKNVDYGAGRLDGYEAIRVAGNFRGNNIDVPNHYYISGYLP-GSRYSDTWTFNAT 478
                                                                339 QAGKPLKISLVWSDAPGSTTASLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNV 398
                                                                                                               243 HDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPK--PSLLKAALIAGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADVGLGFPNGNQGWGRVTLDKSL---NVAFVNETSPLSTSQKATYSFTAQAGKPLKISLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
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STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Write DSM 3638 / ATCC 43587 / JCM 8422;
I'The complete Sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0008233; F:peptidase activity; IEA.
R GO; GO:0008233; F:peptidase activity; IEA.
R GO; GO:0006289; F:subtilase activity; IEA.
R GO; GO:0006289; F:protecolysis and peptidolysis; IEA.
R GO; GO:0006289; Peptidase_S8.
R PEAN: PRO082; Peptidase_S8.
R PRINTE; PS00135; SUBTILASE ASP; I.
R PROSITE; PS00137; SUBTILASE HIS; I.
R PROSITE; PS00138; SUBTILASE SER; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 654;
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SEQUENCE 654 AA; 70230 MM; ICB145A5F505DB34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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29.5%; Pred. No. 3.8e-15;
ive 56; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                           654 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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522 ETITILPSQTGTYYVKVYSY 541
                                                                                                                                                                                                     399 ENVFINAPOSGTYTVEVOAY
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(TrEMBLrel. 21,
(TrEMBLrel. 24,
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Matches 127; Conserv
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NCBI_TaxID=2261;
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01-JUN-2002 (
01-JUN-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 VQNKDVYGIKVINLSLGISTSSDGIDSTSLAVNRAVDSGIVVVVAAAGNSGPAKYTIGSPG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 TAKNALTVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSL 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVGLGFPNGNQGWGRVTLDKSLNVA-------FVNETSPLSTSQKATYSFTA- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 TIPYDDNGHGTHVASIAAGTGAGNSFYKGVAPDALLVGIKVLDANGSGSMSTVTAGIDWA 261
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=2192816. PubbMed=11997336;

A Chen Y., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Bao Q., Tian Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

A Chen Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

A Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12.689-700(2022).

EMBL; AE013049; F.calcium ion binding; IEA.

GO; GO:0006509; F.calcium ion binding; IEA.

GO; GO:0006233; F.peptidase activity; IEA.

GO; GO:0006289; F.subtilase activity; IEA.

GO; GO:0006289; F.subtilase activity; IEA.

GO; GO:0006209; Peptidase_S8.

InterPro; IPR007280; PPC.

R InterPro; IPR00920; Protease_inhib.

R Ffam; PF00151; PPC; I...

R Pfam; PF00151; PPC; I...
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Best Local Similarity 30.2%; Pred. No. 1.1e-15;
Matches 133; Conservative 65; Mismatches 162; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
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SEQUENCE 561 AA; 59968 MW; BA9C5C52F7083A18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          561 AA
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PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE ERR; 1.
                                                                                                                                                                                                                                                                                                                               01-00M-2002 (TrEMBLrel, 21, Creat 01-00W-2002 (TrEMBLrel, 21, Last 01-0CT-2003 (TrEMBLrel, 25, Last Subtilisin-like serine proteases
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                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=119072;
                                                                           : |
VVI 830
                                   LAI 431
                                   429
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RESULT 11

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113 LFSQAYSAGARIHTNSWGA------PVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGP 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 VEADLADSTAQIGAPRAWAGGNTGQGVEVAVLDTGVDAG-----HPDLADRIAARQSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 RINNANDPNGHGTHVAGSVLGNAT----NKGMAPQANLVPQSIMDSGGGLGGLPANLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=A3[2] / M145;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C. W., Collins M.,

Franch A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Rubbinowitsch E., Rajandream M.A., Rutherford K., O'Neil S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.6%; Score 374.5; DB 16; Length 1239; 29.2%; Pred. No. 1.6e-13; tive 57; Mismatches 180; Indels 95;
                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2),
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.,
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1239 AA; 128505 MW; 8F5E9AC68EB1260A CRC64;
                                                                                                                                                                                                                                                         Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO: GO:0008233; F: peptidase activity; IEA.
GO: GO:0004289; F: subtilase activity; IEA.
GO: GO:0004289; F: subtilase activity; IEA.
GO: GO:0006508; F: proteolysis and peptidolysis; IEA.
InterPro: IPR003137; PA.
InterPro: IPR00329; Peptidase_S8.
Ffam; PF00225; PA; 1.
Pfam; PF00232; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00134; SUBTILASE_HS; 1.
PROSITE; PS00137; SUBTILASE_HS; 1.
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coelicolor A3(2).";
Nature 477:141(2002).
EMBL; AL999130; CACO1588.1; --
HSSP; Q99405; 1MPT.
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                                                                                                                      Streptomyces coelicolor
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Matches 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE 1239 AA
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=1902;
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Saunders D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 EPYDD-NGHGTHCAGDAAGNGALSDGQYQGPAPDANLVGVKVLNKTGS-GSLSTVIEGID 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 WCIQNQSKYNINIL---SLSLGSDATEPAEGDPVVNAVET-----AWDNGMVVCVAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GNEGPGSGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 MAPGTYILSARS--SLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGV 277
                     ---GFEKVGYYNPTDG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKIT -- ALYALGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 NNANDPNGHGTHVAGSVLGNAT----NKCMAPQANLVFQSIMDSGGGLGGLPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NLOTLFSQAYSAGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAA
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=HTBB31 / DSM 14371 / JCM 11309;
STRAIN=HTBB31 / DSM 14371 / JCM 11309;
MEDILINE=22220767;
Takami H., Takaki Y., Uchilyama I.;
Takami H., Takaki Y., Uchilyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                              Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.7%; Score 377; DB 16; Length 430; 34.7%; Pred. No. 2.8e-14; ive 44; Mismatches 122; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 30:3927-3935(2002).

BMBL; AP004661; BA1433.1;
GG GO:0004289; F:subtilase activity; IEA.
GG; GO:0006508; P:subtilase and peptidolysis; IEA.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR00081; Peptidase_S8; 1.
PRNINTS; PR00723; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_ERR; 1.
COMPLETE proceeme.
SEQUENCE 430 AA; 45838 MW; 6D09A99BBCIE310F CRC64;
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                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                   473 WDNAN-----SDLDLYLYDPNGNQ-VDYSYTAYY---
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 118; Conservative
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                                                            410 TYTVEVQAYN 419
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514 TWTIKVVSYS 523
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01-MAR-2003 (
01-MAR-2003 (
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Query Match

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Q9FBZ4 Q9FBZ4;

Q9FBZ4 ID Q9

RESULT 12

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-----VDATDILAPFSSQGPRVDGALKPEITAPGV 432
                                                                                                                                                                                                                                                                                              SFTAQAGKPLKISLVWSDAPGST------TASLTLVNDLDLVITAPNGTKYV 380
332 MEWAAVERHAKIVUMMSLGSGEQSDGSDPM-----SRAVDRLSAQTGALFVVAAGNGGE 384
                                                                                                                                                                                                                  285 KAAL---IAGAADVGLGFPNGNQGWGRVTLDKSLN-----VAFVNETSPLSTSQKATY 334
                                                                                                                                                                                                                                                                                                                                    538 INTIGAAVTLELSVAATHAPEGVFRLSASRVTVPAHGTADVTLIIDGS---GSAGGRAYS 594
                                                          GSGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGT 224
                                                                                                                                      225 YILSARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLL 284
                                                                                                                                                                          433 GILAA-----NSSFAAGGNGAYOSLSGTSMATPHVAGAAALL------AAARPDLS 477
                                                                                                                                                                                                                                         :|| :| :| :| :| CSALKDVLASSSHRTPRYDAPFQAGSGRVDVDADAVRAGVYASATAYAPGSSPGPVRRLVTY
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MRDLINE=21996440, PubMed=12000953;
MRDLINE=21996440, PubMed=12000953;
MRDLINE=21996440, Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., Dateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Stabbinowletch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kleser H.M., Denapaite D., Bichner A., Cullum J., Kinashi H., Hopwood D.A., Ast of ordered cognids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                              GNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNVPVSPQTFSL
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STRAIN-A31(2),
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Putative secreted peptidase.
SCO7176 OR SCSA11 04C.
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MEDLINE=97000351; PubMed=8843436;
                                                                                  |||||:|:||||||:|:
385 -AGSIGAPGVATSALTVGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 417:141-147(2002).
EMBL, AL939130, CAC01576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                        GNICEGVGVAVLDIGVDAG-----HPDFAGRIAATASFVPDQDVIDRNGHGTHVASIVA 288
                                                                                                                                                                                                                                                                                                                                                                                                 127 NSWG-APVNGAYTTD--SRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                             342 MSLGDSPTDG---TDPLSEAVNWLSAETGALFVVAAGNSGPEAYTVGTPAAADAALTVGA 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 VNG---PGKG-----VDQLADFSSRGPRVGDNAVKPDLTAPGVGVLAARSRYAPEG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 NQCWGRVTLDKSLNV-----AFVNETSPLSTSQ--KATYSFTAQAGKPLKISLVWSDA
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                   Length 1253;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                        1253 AA; 130971 MW; AA69B417EFEEDB89 CRC64;
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SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
           GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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Last annotation update)
                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                  ; Score 367.5; DB 16;
; Pred. No. 4.1e-13;
60; Mismatches 171;
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NCBI_TaxID=33903;
                                                  InterPro: IPR003137, PA.
InterPro: IPR003137, PA.
InterPro: IPR002039, Peptidase_S8.
Pfam, PP00082, Peptidase_S8, 1.
Pfam, PP00082, Peptidase_S8, 1.
PR.NSTE, PR00723, SUBTILIASE ASP, 1.
PROSITE, PS00137, SUBTILIASE ASP, 1.
PROSITE; PS00137, SUBTILIASE_HIS; 1.
Complete proceome.
SEQUENCE 1253 AA, 130971 MM; AA691
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28.9%;
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25,
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Best Local Similarity 28.9
Matches 140; Conservative
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01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Q82BI4;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1887;
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                                                                                                                                                                                                     MEDLINE=97144528; PubMed=8990295;
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                                                                                                                                                                                                                                                                                                         Streptomyces albogriseolus.
                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 TLFSQAYSA---GARIHTNSWGAPVNGAYTTD--SRNVDDYVRKNDMTILFAAGNEGPGS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22808306; PubMed-1269562;
Ikeda H., Ishikawa J., Hanamoro A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VKADVAQNN------FGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALG
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitiis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.8%; Score 355; DB 16; Length 1208;
.larity 31.7%; Pred. No. 2.1e-12;
Conservative 51; Mismatches 151; Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1208 AA; 125548 MW; E650B5E3AEB5312B CRC64;
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Last annotation update)
                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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Best Local Similarity
Matches 126; Conserv
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SEQUENCE 1208 AA
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ID P9568
AC P9568
DT 01-MADT 01-MADT 01-MADT 01-MADT 01-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 05-MADT 
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131 A-----PVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAITVGA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 NQGWGRVTLDKSLNVAFVNETSPLS------TSQKATYSFTAQAGKPLKISLV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 GYDGKGVKIAVLDTGVD-----ATHPDLKGQVTASKNFTSAPTTGDVVGHGTHVASIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 TENLRPSFGSYADNINHVAQFSSRGP-TRDGRIKPDVMAPGTYILSARSSLAPDSSFWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 HDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 ATGPKGKAAPAGFFTLGASTLTVPANGTASV--DVTADTRLGGAVDGTYSAYVVATGAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTNNANDPNGHGTHVAGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 GMDTPETDPLEAA-----VDKLSAEKGILFAIAAGNEGPQS--IGSPGSADSALTVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 G-----NATNKGMAPQANLVFQSIMDSG--GGLGGLPANLQTLFSQAYSAGARIHTNSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 EGGSGRVQVDKAITQTVIAEPVSLSFGVQQWPHADDKPVTKKLTYRNLGTEDVTLKLTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1102;
Suzuki M., Taguchi S., Yamada S., Kojima S., Miura K., Momose "A novel member of the subtilisin-like protease family from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Protease, Serine_protease.
SEQUENCE 1102 AA, 114128 MW; F954AD2590F5559E CRC64;
                                                                                                                                                                                                                     MENOPS; 508.04; 0.094.

MENOPS; 508.069; --

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:0006208; F:subtilase activity; IEA.

InterPro; IRR022660; GH_BNR.

InterPro; IRR022660; GH_BNR.

Pfam; PRO0082; Peptidase_S8; 1.

Pfam; PRO0082; Peptidase_S8; 1.

PRINTS; PRO0136; SUBTILASE_MSP; 1.

PROSITE; PS00137; SUBTILASE_MSP; 1.

PROSITE; PS00136; SUBTILASE_HIS; 1.

PROSITE; PS00136; SUBTILASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
15.2%; Score 341.5; DB 2;
Best Local Similarity 30.2%; Pred. No. 1.1e-11;
Matches 132; Conservative 51; Mismatches 181;
                                                                                                                                     88
                                                                        J. Bacteriol, 179:430-438(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
EMBL; D83672; BAA12040.1; -.
HSSP; P00782; 2SBT.
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16;

372

242

421

321

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

March 31, 2004, 15:58:03 ; Search time 47.1304 Seconds (without alignments) 2595.843 Million cell updates/sec

US-09-985-689A-7 2252

1 NDVARGIVKADVAQNNFGLY......EVQAYNVPVSPQTFSLAIVH.433 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Result

Description	m50086 Bac	_	380 Ba	190 Bac	Aay17091 Bacillus	081 Bacil	Aam50085 Bacillus	Bacil	. An alka	An al	Baci	Aam50082 Bacillus	8 Bacil	83 Bacil	74 Alkal:	n n	98 Bacil	Aay69207 Amino aci	19 Bacil	90 Baci	30 Subti	Aay21654 Subtilase	21	8	Aaw94836 Hyperther
QI	AAM50086	AAW89547	AAM50080	AAY17090	AAY17091	AAM50081	AAM50085	AAY17089	AAY17087	AAY17088	AAM50084	AAM50082	AAW89548	AAM50083	AAR26274	AAW61495	AAW95698	AAY69207	AAY44619	AAM50090	AAW62230	AAY21654	AAW24121	AAW94840	AAW94836
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Score	25	2252	125.	125.	120.	118.	2116.5	11	90	090	9	9	0	03	03	03	03	2032	2032	1949.5	64	4	m	N	g
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Aaw24122	Aaw94838	Aaw24129	Aaw94841	Aaw24123	Abb09483	Aab81180	Abu07391	Aaw13666	Aaw13667	Aaw13668	Abu11343	Aar27481	Aar87007	Aar87008	Aaw24124	Aaw94839	Abp76735	Abp76678	Aay08471
AAW24122	AAW94838	AAW24129	AAW94841	AAW24123	ABB09483	AAB81180	ABU07391	AAW13666	AAW13667	AAW13668	ABU11343	AAR27481	AAR87007	AAR87008	AAW24124	AAW94839	ABP76735	ABP76678	AAY08471
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522	522	654	654	629	545	1079	1079	520	734	823	1237	806	903	1398	1398	1398	519	19938	669
17.6	17.6	17.6	17.6	17.3	16.4	15.2	15.2	14.5	14.5	14.5	14.3	13.7	13.6	13.6	13.6	13.6	13.2	13.2	12.8
396	396		396	390	369.5	341,5	341.5	327.5	327.5	327.5	323	309	306	306	306	306	297	297	289
56	27	28	53	30	31	32	33	34	3.5	36	3.7	38	66	40	41	42	43	44	45

## ALIGNMENTS

Sumitomo Alkaline protease; detergent; laundry; bleaching; dishwasher. 'n, Bacillus sp alkaline protease protein A-2 fragment Araki Sato T, AAM50086 standard; protein; 433 AA. Hatada Y, Ogawa A, Kageyama Y, Okuda M, Saeki K; 22-NOV-2001; 2001EP-00127851. 22-NOV-2000; 2000JP-00355166. 12-APR-2001; 2001JP-00114048. (first entry) WPI; 2002-437518/47. (KAOS ) KAO CORP. EP1209233-A2. Bacillus sp. 12-AUG-2002 29-MAY-2002. AAM50086; 

New modified alkaline proteases useful in detergent compositions

Claim 5; Page 20-21; 25pp; English.

This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency \$ (34 - 38*) compared to prior art alkaline proteases (31 and 23*). This sequence represents a fragment of the alkaline protease A-2 from Bacillus sp NCIB12513 described in the method of the invention

Sequence 433 AA;

Gaps . 0 Query March
100.0%; Score 2252; DB 5; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.2e-160;
Matches 433; Conservative 0; Mismatches 0; Indels 0;

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1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHBAFRGKITALYALGRTN 60

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EP1209233-A2
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                                    NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
        9
LTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV
                                                    GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT
                                                               GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT
                                                                                              VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW
                                                                                                              ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                           241 ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                                           NGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS
                                                                                                                                                       NGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS
                                                                                                                                                                        LILVNDLDLVITAPNGTKYYGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing.
                                                                                                                                                                                                                                                                                                                   Protease; detergent; surfactant; leather processing; debittering;
                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
34. 208
/note= "prepro region"
209. 641
/note= "mature protein"
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                                                                                                                                                                                                                                                                                                    Bacillus JP170 protease
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N-PSDB; AAV82382.
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This is the amino acid sequence of a novel protease of Bacillus sp. JD170 (NCIB 12513), as deduced from the nucleotide sequence of an isolated gene consequence and solated sequence of an isolated gene at Section 2. The section is protein, including the signal peptide and preprior region, has 77% identity to alkaline protease Y (see AAM89548) from Bacillus. The invention provides vectors, recombinant host cells and methods for the recombinant production of the protease. The protease is used in laundry and dishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the degree of hydrolysis of proteins, degradation of undesired peptides and in enzymatic synthesis of proteins of the senanced stability towards oxidation under alkaline conditions, it has enhanced stability towards oxidation under alkaline conditions, it is towards bleaching agents of the peroxy type. The invention also provides mutant cells in which the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2252; DB 2; ilarity 100.0%; Pred. No. 2.1e-160; Conservative 0; Mismatches 0;
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Page 53-54; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM50080 standard; protein; 434
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Best Local Similarity
Matches 433; Conserv
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                                                                                                                                                                                     This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38$) compared to prior art alkaline proteases (31 and 22$). This sequence represents a fragment of the alkaline protease KP43 from Bacillus sp strain KSW-KP43 which is used to create the modified protease represented in AAMS0091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                               New modified alkaline proteases useful in detergent compositions
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                                                                                                                                                                                                                                                                                                  Length 434;
                                                                                             Sumitomo
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                                                                                                                                                                                                                                                                                                 94.4%; Score 2125.5; DB 5; 93.5%; Pred. No. 3.9e-151; ive 19; Mismatches 8;
                                                                                             Araki
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                                                                                              Sato
                                                                                                                                                                     Claim 1; Page 10-11; 25pp; English
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                                                                                              Kageyama
                    22-NOV-2001; 2001EP-00127851
                                        22-NOV-2000; 2000JP-00355166
12-APR-2001; 2001JP-00114048
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.5:
Matches 406; Conservative
                                                                                                                           WPI; 2002-437518/47.
                                                                                             Ogawa A,
Saeki K;
                                                                        (KAOS ) KAO CORP.
                                                                                                                                                                                                                                                                             Sequence 434 AA;
29-MAY-2002
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                                                                                                      Okuda M,
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AAY17090 standard; protein; 640

(revised) (first entry)

20-MAR-2003 21-JUL-1999

AAY17090;

52555F

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to alkaline proceases produced by strains of Bacillus. The proceases ability to digest casein is not inhibited by older caid and they have a high stability to oxidising agents. The is active over the phrange 4-13 and has the following properties: (a) it is active over the phrange 4-13 and has at least 80% of its optimum activity over the phrange ph 6-12; (b) after 30 minutes at 40 deg; C it is stable over the phrange 6-11; c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proceases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing compositions for use in automatic dishwashers bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                    e protease; Bacillus; casein digestion; oleic acid; enzyme; composition; oxidising agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protease from Bacillus used in washing powders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hitomi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 94.4%; Score 2125.5; DB 2; Local Similarity 93.5%; Pred. No. 6.7e-151; tes 406; Conservative 19; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kubota H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 58-63; 71pp; Japanese.
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                                                                                                                                                                                                                                                                                                        98WO-JP004528
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Bacillus alkaline protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okuda M,
Nomura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-287736/27.
N-PSDB; AAX37278.
                                                                                                                                                                                                                                                                                                                                                                                                                 (KAOS ) KAO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 640 AA;
                                                                                                                                                                                           WO9918218-A1
                                                                                                                                                                                                                                                                                                        07-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                            07-OCT-1997;
                                                                                                                                                                                                                                                   15-APR-1999
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Shikata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1209233-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hatada Y,
Okuda M, S
                                                                                                                                                                                                                                                                                                                                                                                                              AAM50081;
           120
                                    327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to diget casein is not inhibited by oles acidlus. The protease a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; (c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by 809-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
              SVILVNDLDLVIIAPNGIQYVGNDFISPYNDN#DGRNNVENVFINAPQSGTYIIEVQAYN 626
SLTLVNDLDLVITAPNGTXYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                         Alkaline protease, Bacillus, casein digestion, oleic acid, enzyme, washing composition, oxidising agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kageyama Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.2%; Score 2120.5; DB 2; Length 640; 93.3%; Pred. No. 1.6e-150; ive 19; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alkali protease from Bacillus used in washing powders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hitomi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kubota H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese.
                                                                                                                                                 AAY17091 standard, protein, 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saeki K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 63-68; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                  98WO-JP004528
                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-00274570
                                                                               640
                                                    VPVSPQTFSLAIVH 433
                                                                                                                                                                                                                                               Bacillus alkaline protease
                                                                                                                                                                                                      (revised)
(first entry)
                                                                     VPVGPQTFSLAIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okuda M,
Nomura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-287736/27.
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                                                                                                                                                                                                                                                                                                                Bacillus sp.
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21-JUL-1999
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                                                                                                                                                                           AAY17091;
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                        267
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360
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386
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                                                                                                                                                             566
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                                                                                                                                                                                                         WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF
                                                                                                300 PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
                                                                                                                                                      360 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                             TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified alkaline proteases useful in detergent compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alkaline protease; detergent; laundry; bleaching; dishwasher
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus sp KSM-KP9860 alkaline protease protein fragment.
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                                                                                                                                                                                                                                                                                                                                             AAM50081 standard; protein; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Кадеуата
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-2001; 2001EP-00127851.
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12-APR-2001; 2001JP-00114048.
                                                                                                                                                                                                                                                  433
                                                                                                                                                                                                                                                                          627 VPVGPONFSLAIVN 640
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.33
Matches 405; Conservative
                                                                                                                                                                                                                                               420 VPVSPQTFSLAIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogawa A,
Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-437518/47.
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Gaps

1;

NANDINGHGTHVAGSVLGNGSTNKGMAPQANLVFQSIMDSGGGLGGLFGLFSQAYS 326

NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS

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267 61

1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN

Best Local Similarity 93.3 Matches 405; Conservative

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241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLLKAALIAGATDIGLGY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                              WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF
                                                                                                                                                                                                                                                       121 AGARIHTUSWGAPVNGAYTTDSRNVDDYVRKNDMAVLFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                     TVGATENLRPSFGSYADNINHVAQFSSRGPTXDGRIKRDVWAPGTFILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                             PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                            1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                              1 NDVARGIVKADVAQSSYGLYGQQQVVAVADTGLDTGRNDSSMHEAFRGKITAIYALGRTN
                                                                                                                                                                         NANDPNGHGTHVAGSVLGNAT - NKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                                                                                                                                                     120 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                  TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                              Gaps
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                                                434;
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                                                Length
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alkali protease from Bacillus used in washing powders
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                                                DB 5;
                                                                              12;
                                            94.0%; Score 2116.5; DB 5
92.2%; Pred. No. 1.9e-150;
ive 21; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-JP004528
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(first entry)
                                                               Best Local Similarity 92.2%
Matches 400; Conservative
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Nomura M;
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N-PSDB; AAX37277.
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                  Sequence 434 AA;
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Shikata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1999.
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21-JUL-1999
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                                                Query Match
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                                                                                                                            179
                                                                                                                                           AGARIHTINSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
                                                                                                                                                                                        239
                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                 PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA 359
                                                                                                                                                                                                                                                                                                                                  PNGNQGWGRVTLDKSLNVAYVNESSALSTSQXATYTFTATAGXFLKISLVWSDAPASTTA 360
                                                                                                                                                                                                                                                                                                                                                                           SLILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 419
                                                                                                                                                                                                                                                                                                                                                                                              SVTLVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN 420
                                                                                                                                                                                                                                                  WANHDSKYAYMGGISMAIPIVAGNVAQLREHFVKNRGVIPKPSLLKAALIAGAADVGLGF 299
   9
                                 9
                                                                                           NANDTNGHGTHVAGSVLGNGATNKGNAPQANLVFQSIMDSSGGLGGLPSNLQTLFSQAFS
                                                                                                                                                                                                                                                                      NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                   NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                           NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                                         AGARIHTINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                                                                                                                                      TVGATENLRPSFGSYADNINHVAQPSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                   TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTYILSARSSLAPDSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alkaline protease; detergent; laundry; bleaching; dishwasher.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus sp alkaline protease protein A-1 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Araki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ė
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified alkaline proteases useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 18-19; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM50085 standard; protein; 434 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-2001; 2001EP-00127851
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12-APR-2001; 2001JP-00114048.
                                                                                                                                                                                                                                                                                                                                                                                                                                           VPVSPQTFSLAIVH 433
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Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-437518/47.
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The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 9+6.12, (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11, (c) its isoelectric point is 8.9-9.1, (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGS. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidiaing agents allows the bleaches. The present sequence represents an alkaline protease of the invention. (Updated on 20-MAR-2003 to correct DR field.)

    639
/note= "all residues indicated as Xaa are arbitrary amino
acids"

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                                                                                                                                                                                                                                                                                                     J, Kageyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                           Alkali protease from Bacillus used in washing powders
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                                                                                                                                                                                                                                                                                                     Hitomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
91.5%; Score 2060.5; DB 2;
Best Local Similarity 91.7%; Pred. No. 5.1e-146;
Matches 398; Conservative 12; Mismatches 23;
                                                                                                                                                                                                                                                                                                     Kubota H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 47-50; 71pp; Japanese.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       Saeki K,
                                                                                                                                                                                  98WO-JP004528
                                                                                                                                                                                                                         97JP-00274570
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Nomura M;
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    Key
Misc-difference
                                                                                                                                                                                  07-OCT-1998;
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                                                                                                                                                                                                                                                                  (KAOS ) KAO
                                                                                                                                                                                                                                                                                                       Takaiwa M,
Shikata S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325
                                                                            Bacillus. The processes ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline processe of the invention has the following agents. The is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11, (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11, c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has noclecular weight about 43,000 by SDS-PAGE. The alkaline processes can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NANDPNGHGTHVAGSVLGN-ATNKGMAPOANLVFQSIMDSGGGLGGLPANLQTLFSQAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVMNRGVTPKPSLLKAALIAGAADVGLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNERPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij,
                                                                                                                                                                                                                                                                                                                                                                                                                Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alkaline protease, Bacillus, casein digestion, oleic acid; washing composition, oxidising agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An alkaline protease sequence from Bacillus species.
                                                                                                                                                                                                                                                                                                                                                                                                              93.7%; Score 2110.5; DB 2; 93.1%; Pred. No. 9e-150; ive 18; Mismatches 11;
                          Disclosure; Page 53-58; 71pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 93.19
Marches 404; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 639 AA;
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21-JUL-1999
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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease SD-521 from Bacillus sp strain SD-521 (FERM BP-11162) described in the method of the
                                                                                                                                                                                                                                                               387 TVGATENIKPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTXILSARSSLAPDSSF
                                                                                                                                                                                                              (FERM BP-11162) alkaline protease protein fragment.
                                         AGARIHINSWGAPVNGAYITDSRNVDDYVRKNDMILFAAGNEGPGSGTISAPGTAKNAI
                                                             AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEXPNGGTISAFGTAKNAI
                                                                                           180 TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
                                                                                                                                            WANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF
                                                                                                                                                               PNGNQGWGRVTLDXSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA
                                                                                                                                                                                                                                                 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified alkaline proteases useful in detergent compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sumitomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alkaline protease; detergent; laundry; bleaching; dishwasher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2044;
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                                                                                                                                                                                                                                                                                                                                                                                               AAM50084 standard; protein; 433
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12-APR-2001; 2001JP-00114048.
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                                                                                                                                                                                                                                                                                                      VPVSPQTFSLAIVH 433
                                                                                                                                                                                                                                                                                                                                VPVGPOXFSLAIVN 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2002 (first entry)
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Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-437518/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SD-521
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                                                                                                                                                                                                                                                                                                         1. .640 ^{\circ} /note= "all residues indicated as Xaa are arbitrary amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NANDPNGHGTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to exidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease of the invention. (Updated on 20-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                         Alkaline protease, Bacillus, casein digestion, oleic acid, enzyme, washing composition, oxidising agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kageyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease from Bacillus used in washing powders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ה,
                                                                                                                                                                                                  An alkaline protease sequence from Bacillus species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hitomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.5%; Score 2060.5; DB 2; 91.7%; Pred. No. 5.1e-146; ive 12; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kubota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 50-53; 71pp; Japanese.
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                          AAY17088 standard; protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saeki K,
                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-00274570
                                                                                                                                                                                                                                                                                                                                                                                                               98WO-JP004528
                    433
                                             639
                                                                                                                                                              (revised)
(first entry)
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                                    VPVGPQXFSLAIVN
                    VPVSPQTFSLAIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okuda M,
Nomura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-287736/27.
N-PSDB; AAX37278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAOS ) KAO CORP
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                                                                                                                                                                                                                                                                                                                                                                                                               07-0CT-1998;
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                                                                                                                                                                                                                                                                                                                                                            WO9918218-A1
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                                                                                                                                                            20-MAR-2003
21-JUL-1999
                                                                                                                                                                                                                                                                  Bacillus sp
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                   420
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Shikata
                                           626
                                                                                                                                     AAY17088;
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Matches
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361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNMMDGRNNVENVFINAFQSGTYTIEVQAYNV 420
                                                                                                                                                                                                                                                                                                                            VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                            NGNQGWGRVTLDKSLNVAPVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease E-1 from Bacillus sp strain D6-(FERM-P1592) described in the method of the invention
                                                                                                                                                                                                                              121 GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV 420
                                                                                                                                                                                                          NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
                                                                                                                                                                                                                                                                                                                                                                                     ANHOSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                                                                                                                                                                                                                                                      VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                                    1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                  1 NDVARGIVKADVAQNNFCLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                    GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protease from Bacillus subtilis LC20 - useful in laundry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detergent; surfactant; leather processing;
                                                                                              Length 433;
                                                                                                                         Indels
                                                                                          90.6%; Score 2040; DB 5;
llarity 88.9%; Pred. No. 1e-144;
Conservative 24; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus sp. alkaline protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alkaline protease Y;
debittering; flavour.
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                                                                                                       Best Local Similarity
Matches 385; Conserv
                                                                   Sequence 433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-1997;
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                                                                                              Query Match
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                                                                                                                                                                                                                                             181 VGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                     ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
                                                                                                                                                                                                                                                                                                                                                                                                                     YTLVNDLDLVIIAPNGOKYVGNDFSYPYDNWDGRNNVENVFINAPOSGTYTIEVOAYNV
                                                                                                                                                                                                                         VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                             NGNOGWGRVTLDKSLNVAFVNBTSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS
                                                                                                                                                                                                                                                                                                                                                               LTLVNDLDLVITAFNGTKYVGNDFTAFYDNNWDGRNNVENVFINAFQSGTYTVEVQAYNV
                                                                                                                                                                                     ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                    1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                           NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                             NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA
                                                                                                                                                                     GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAIT
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D6-(FERM P1592) alkaline protease protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alkaline protease; detergent; laundry; bleaching; dishwasher.
                           Indels
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                           23;
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             5.2e-145;
            Pred. No. 5.26
; Mismatches
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89.1%; Fit. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; protein; 433
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12-APR-2001; 2001JP-00114048
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                          Conservative
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Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-437518/47
         Best Local Similarity
Matches 386; Conserv
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                                          This is the amino acid sequence of a Bacillus sp. alkaline protease Y that is said to have good alkali and surfactant resistance and improved detergency. It shows 7% identity to a newly isolated protease (see AAW8547) of Bacillus sp. JP10 (NCIB 12513). The invention provides cortors, recombinant host cells and methods for the recombinant proteases. The protease are used in laundry and ishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the for leather processing, as well as for debittering and enhancing the chrough hydrolysis of proteins, degradation of undesired peptides and in enzymatic synthesis of proteins, rey towards bleaching agents of the corroxy type. The invention also provides mutant cells in which the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
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                                                                                                                                                                                                                                                                                                                                                                                                      GARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGFGSGTISAPGTAKNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                             636;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                             Length
for leather processing
                                                                                                                                                                                                                                                           90.5%; Score 2038; DB 2;
88.9%; Pred. No. 2.5e-144;
ive 25; Mismatches 23;
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                       Claim 3; Page 55-56; 77pp; English
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  detergents and
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Best Local Similarity
Matches 385; Conserv
                                                                                                                                                                                                                                     Sequence 636 AA;
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dishwashing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
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                                                                                                                                                                                                                                                                   New modified alkaline proteases useful in detergent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.3%; Score 2033; DB 5; Best Local Similarity 88.7%; Pred. No. 3.5e-144; Matches 384; Conservative 25; Mismatches 24;
                                                                                                                                                                                  Araki
                                                                                                                                                                                    Sato T,
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200JJP-00114048
                                                                22-NOV-2001; 2001EP-00127851
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Saeki K;
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                                                                                                                                                (KAOS ) KAO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 433 AA;
EP1209233-A2
                                                                                                 22-NOV-2000;
                                                                                                                 12-APR-2001;
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                                29-MAY-2002
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Okuda M, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 YTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTXIIEVQAYNV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NANDPNGHCTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 NGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTAS 360
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                                        Alkali resistance; surface active agent resistance; detergency improver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN
                                                                                                                                                                                                                                                                                                                                                                                 DNA coding alkali-protease Ya enzyme - has good alkali and surfactant resistance and improves detergency.
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90.2%; Score 2032; DB 2; Length 4:
Best Local Similarity 88.7%; Pred. No. 4.1e-144;
Matches 384; Conservative 25; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 1; 17pp; Japanese.
                                                                                                                                                                                                     90JP-00327110.
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Alkali-protease Ya enzyme.
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                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ27516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 433 AA;
                                                                             Bacillus sp. Y.
                                                                                                                      JP04197182-A.
                                                                                                                                                                                                                                          28-NOV-1990;
                                                                                                                                                                                                     28-NOV-1990;
                                                                                                                                                            16-JUL-1992
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Search completed: March 31, 2004, 16:04:34 Job time : 48.1304 secs

8, Appli 16, Appli 2, Appli 44, Appli 4, Appli 4, Appli 4, Appli 11, Appli 11, Appli 11, Appli 11, Appli

Sequence 8, M. Sequence 6, M. Sequence 14, M. Sequence 4, M. Sequence 4, M. Sequence 4, M. Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 5, M.

Sequence

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1 NDVARGIVKADVAQNNFGLYGGGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 2252; DB 2; Length 641; Best Local Similarity 100.0%; Pred. No. 1.8e-174; Matches 433; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-873-479-42

Sequence 42, Application US/08873479
Sequence 42, Application US/08873479
Sequence 42, Application US/08873479
Sequence 42, Application Application Application Application Application And Alan Application Lynne, Christianson
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES:
MURPER OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES:
ADDRESSEE: No. 58917010 No. 5891701disk of No. 5891701th ASTREET: 405 Lexington Avenue
CITY: New York
STREET: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCREATING SYSTEM: DOS SOFTWARE: PASALSED for Windows Version 2.0 SOFTWARE: PastSED for Windows Version 2.0 CURBENT APPLICATION NUMBER: US/08/873,479 FILING DATE: 12-UN-1997 CLASSIFFCATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Agris, Cheryl H REGISTRATION NUMBER: 34,086 RESTRATION NUMBER: 34,086 REFERENCE/DOCKET NUMBER: 5251.000-US TELEPHONE: 212-867-0123
                                                        US-09-445-472-6
US-08-760-532-18
US-08-873-479-44
US-08-873-479-44
US-08-24-021-4
US-08-28-021-4
US-08-585-798-4
US-09-585-798-4
US-09-585-798-4
US-09-585-798-4
US-09-585-798-4
US-09-585-798-4
US-08-566-369-11
US-08-566-369-11
US-07-76-691G-5
US-08-254-021-5
US-08-254-021-5
                                        -08-894-818B-8
                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Con
OPERATING SYSTEM:
10174
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Sequence 6, Appli
                                                                                                                                       March 31, 2004, 15:59:39 ; Search time 13.9892 Seconds (without alignments) 1597.947 Million cell updates/sec
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Sequence 4, Al
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1 NDVARGIVKADVAQNNFGLY.......EVQAYNVPVSPQTFSLAIVH 433
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1. /cgn2 6/ptodata/2/iaa/5B COMB.pep:*

3. /cgn2 6/ptodata/2/iaa/6A COMB.pep:*

1. /cgn2 6/ptodata/2/iaa/6B COMB.pep:*

2. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*

2. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*

3. /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-104-62A-4
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327 AGARIHTUSWGAAVNGAYTTDSRNVDDYVRKNDWTILFAAGNBGPNGGTISAPGTAKNAI 386
                                                                                                                                                                                        240 WANHDSKYAYMGGTSMATFIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF 299
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                                                                                                                                                                                                                        447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KAGENAMA, YASUSHI
APPLICANT: KAGENAMA, YASUSHI
APPLICANT: KAGENAMA, SHITSUW
APPLICANT: NOWIRA, MASAFUMI
I TITLE OF INVENTION: ALKALINE PROTEASE
FILE REPERENCE: 0327-0322-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DFT/JP98/04528
PRIOR APPLICATION NUMBER: JP9-106-08
NUMBER: OF SEQ ID NOS: 24
SEQ ID NOS: 24
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SEQ ID NOS: 24
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Patent No. 6376227
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MITSUYOSHI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SABKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
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209 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 268
                                                      NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
                                                                                                          NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 328
                                                                                                                                                        GARIHINSWGAPVNGAYTIDSRNVDDYVRKNDMILLFAAGNEGPGSGILSAPGTAKNAIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TAKANA, MIKIO
APPLICANT: TAKANA, MIKIO
APPLICANT: OKUDA, MITGITYOSHI
APPLICANT: SHEKI, KATSUHISA
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, MASAFUMI
TITLE OF INVENTION: 0.227-0.032-0.0CT
CURRENT APPLICATION NUMBER: DCO,09-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR APPLICATION NUMBER: JP 9-274570
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09509614A Patent No. 6376227 GENERAL INFORMATION:
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Matches 406; Conservative
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US-09-509-814A-6
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360 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 419
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GENERAL INFOGRATION:
APPLICANT: TAKANA, MIKIO
APPLICANT: OKUDA, MITSIYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBCAT, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SHIKSUM
APPLICANT: SHIKATA, SHIKSUM
APPLICANT: SHIKATA, SHIKATA
ITILE NEFERENCE: 0327-0822-0PCT
CURRENT APPLICATION NUMBER: US/09/509, 614A
CURRENT APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
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LOCATION: (32).
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (46)...(46)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (47)...(47)
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
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NAME/KEY: misc feature
LOCATION: (105). (105)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (128).. (128)
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LOCATION: (23) ... (23)
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: (29)...(29)
OTHER INFORMATION: Xaa is any amino acid
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NAME/KEY: misc feature
LOCATION: (102)..(102)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09509814A; Patent No. 6376227
                                                                                                                                                                                       420 VPVSPQTFSLAIVH 433
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ORGANISM: Bacillus sp.
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                                                                                                                                                                                                                                                                                                       360 SLTLVNDLDLVITAPNGTKYVGNDFTAPYDNNADGRNNVENVFINAPQSGTYTVEVQAYN 419
                                                                                                                                                                                                                                                                                                                                                     61 NANDPNGHCTHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYS 119
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240 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKDSLLKAALIAGAADVGLGF 299
                                                                                                                                                          300 PNGNQGWGRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVWSDAPGSTTA 359
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Best Local Similarity 93.1%; Pred. No. 5.4e-163;
Matches 404; Conservative 18; Mismatches 11; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TAKANA, MIKIO
APPLICANT: GKUDA, MITSUYOSHI
APPLICANT: GREKI, KATSUHISA
APPLICANT: GREKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA, SHIKATA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 VPVSPQTFSLAIVH 433
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LENGTH: 639
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OTHER INFORMATION: Xaa	NAME/KEY: misc_feature LOCATION: (130)(130) OTHER INFORMATION: Xaa is NAME/KEV: misc_feature	LOCATION: (131). (131) OTHER INFORMATION: Xaa	NAME/ABI: MISC_LEGACULE LOCATION: (132) OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (133). (133) OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (146)(146) OTHER INFORMATION: Xaa NAME/KEY. misc feature	LOCATION: (148).(148) OTHER INFORMATION: (148) NAME/KEY: misc feature	LOCATION: (160)(160) OTHER INFORMATION: Xaa NAME/KEY: misc_feature	LOCATION: (165)(165) OTHER INFORMATION: Xaa	NAME/ASI: MISC LEGALUE LOCATION: (172)(172) OTHER INFORMATION: Xaa NAME/KRY. misc feature	LOCATION: (183)(183) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (187)(187) OTHER INFORMATION: Xaa	NAME/KEY: MISC FEATURE LOCATION: (188)(188) OTHER INFORMATION: Xaa	NAME/KEY: misc_feature LOCATION: (189)(189) OTHER INFORMATION: Xaa	NAME/KEY: misc_feature LOCATION: (194)(194) OTHER INFORMATION: Xaa	NAME/KEY: misc reature LOCATION: (286)(286) OTHER INFORMATION: Xaa	NAME/KEI: MISC LEACUTE LOCATION: (306). (306) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (324)(324) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (369)(369) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (431)(431) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (501)(501)	OTHER INFORMATION: Xaa NAME/KEY: misc feature LOCATION: (531)	OTHER INFORMATION: Xaa NAME/KEY: misc feature	LOCATION: (541)(541) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (584)(584) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (591)(591) OTHER INFORMATION: Xaa

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               CCATION: (592)...(592)

COTHER INFORMATION: Xaa is any amino acid

MAME/KEX: misc_feature

LOCATION: (594)...(594)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: (595)...(595)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: (596)...(596)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: (611)...(611)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: (632)...(632)

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COCATION: (632)...(632)
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APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATA, SHITSUM
APPLICANT: NOMURA, MAGAFUMI
TILLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0227-0892-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
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US-09-509-814A-2
; Sequence 2, Application US/09509814A
; Patent No. 6376227
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APPLICANT: TAKAINA, MIKIO
APPLICANT: OKUDA, MITSUVOSHI
APPLICANT: SABEL, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, UNN
APPLICANT: SHIKATA, SHIKATA, SHIKATA, APPLICANT: SHIKATA, SHIKATW
APPLICANT: NOMURA, MASAFUMI
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7%
Matches 398; Conservative
NAME/KEY: misc_feature
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	Gaps
	640;
	Length Indels
	; DB 4; 2e-159; s 23;
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LOCATION: (166)(166)  MAME/KST misc feature LOCATION: (1737)(173)  MAME/KST misc feature LOCATION: (1847)(189)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1895)(189)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(189)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(189)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1997)(190)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1975)(1937)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1975)(1937)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1975)(1937)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1975)(1937)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1975)(1937)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1987)(1993)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1997)(1993)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1997)(1993)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1997)(1993)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1997)(1993)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1997)(1993)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(1993)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(1995)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(1995)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(1995)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(1995)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1995)(1995)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1996)(1996)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1996)(1996)  OTHER INFORMATION: Xaa i MAME/KST misc feature LOCATION: (1996)(1996)  OTHER MISC feature LOCATION: (1996)(1996)  OTHER MISC feature LOCATION: (1996)(1996)  OTHER MISC feature LOCATION: (1996)(1996)  OTHER MISC feat	) ~ ~ ~ ~

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MOLECULE TYPE: protein ORIGINAL SOURCE:
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linear
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                                                                267 NANDINGHGIHVAGSVIGNGXINKGMAPQANIVFQSIMDSXGGIGGIPSNIQTIFSQAXS 326
                                 NDVARGIVKADVAQNNFGLYGQGQIVAVADIGLDIGRNDSSMHEAFRGKITALYALGRIN 60
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWART PAPLICATION DATA:
APPLICATION NUMBER: US/09/104,623A
FILING DATE: 25-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT THORMATION:
NAME: ROASE, Carol
REGISTRATION NUMBER: 36,993
REFERRENCE/DOCKET NUMBER: 5256.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TYPE: amino
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ZIP: 101
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                                                               Query March 90.2%; Score 2032; DB 4; Length 4 Best Local Similarity 88.7%; Pred. No. 7.3e-157; Matches 384; Conservative 25; Mismatches 24; Indels
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Patent No. 6416756

GENERAL INFORMATION:

APPLICANT: Olsen, Annethe

TITLE OF INVENTION: A modified Enzyme for Skin Care

TITLE OF INVENTION: A modified Enzyme for Skin Care

TITLE OF INVENTION: A modified Enzyme for Skin Care

TITLE APPLICATION NUMBER: US/09/019,532B

CURRENT FILING DATE: 1998-02.05

EARLIER APPLICATION NUMBER: 0038/97

EARLIER FILING DATE: 1997-01-10

EARLIER FILING DATE: 1997-06.25

EARLIER FILING DATE: 1997-06.25

EARLIER FILING DATE: 1997-06.25

EARLIER FILING DATE: 1997-06.25

EARLIER FILING DATE: 1998-01-12

NUMBER OF SEQ ID NOS: 5

SOFTWARE FREEDOM FOR WINDOWS VETSION 3.0
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90.2%; Score 2032; DB 4;
Best Local Similarity 88.7%; Pred. No. 7.3e-157;
Matches 384; Conservative 25; Mismatches 24;
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STRAIN: Bacillus sp. Y
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121 GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT 180
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APPLICANT: Slowe, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58917010 No. 5891701disk of No. 5891701th America
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCHES FASTEM: DOS
SOCHES FASTEM: DOS
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ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

MEDIUM TYPE: DISKette

MEDIUM TYPE: DISKette
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amino acid
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Best Local Similarity 88.7
Matches 384; Conservative
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LENGTH: 635 amino acid
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TOPOLOGY:
US-08-873-479-43
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                                                                                           1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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Sequence 4, Application US/09338746

Sequence 4, Application US/09338746

GENERAL INFORMATION:
APPLICANT: Descent Heinz-Josef
APPLICANT: Peacum, Tine A.
TITLE OF INVENTION: A Polypeptide-Polymer Conjugate
TITLE OF INVENTION: A Polypeptide-Polymer Conjugate
TITLE OF INVENTION: A Polypeptide-Polymer Conjugate
TITLE OF INVENTION: A Polypeptide-Polymer Congress
TITLE OF INVENTION: A Polypeptide-Polymer Congress
CURRENT APPLICATION NUMBER: US/09/338,746
CURRENT FILING DATE: 1999-06-23

EARLIER APPLICATION NUMBER: PA 1998 00809

EARLIER APPLICATION NUMBER: 60/091,461

SARIER FILING DATE: 1998-07-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FatlSEQ for Windows Version 3.0

SEQ ID NO 4.
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88.7%; Pred. No. 7.3e-157;
tive 25; Mismatches 24;
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Best Local Similarity 88.73
Matches 384; Conservative
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US-09-196-281-13
US-09-196-281-13
; Sequence 13, Application US/09196281A
; Patent No. 6605458
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hansen, Peter K.
APPLICANT: Bauditz, Peter K.
APPLICANT: Mixkelsen, Frank
; TITLE OF INVENTION: Protease Variants And Compositions
; TITLE OF INVENTION: Protease Variants And Compositions
; CURRENT APPLICATION: NUMBER: US/09/196,281A
; CURRENT APPLICATION NUMBER: 1332/97
; EARLIER APPLICATION NUMBER: 1332/97
; RARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.2%; Score 1649; DB 4; Length 3 100.0%; Pred. No. 6.2e-126; ive 0; Mismatches 0; Indels
                                                                                                                                                                                 US-09-515-150A-10

| Sequence 10, Application US/09515150A |
| Sequence 10, Application US/09515150A |
| Patent No. 6558938 |
| GENERAL INFORMATION: |
| APPLICANT: Hansen, Peter |
| APPLICANT: Andersen, Kim |
| APPLICANT: Andersen, Kim |
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| APPLICANT: Andersen, Kim |
| SOFTWARE: Patentin version 3.1 |
| SOFTWARE: Patentin version 3.1 |
| SOFTWARE: Patentin version 3.1 |
| SOFTWARE: Bacillus |
| TYPE: PRT |
| SOGANISM: Bacillus |
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| SOFTWARE: PATENTING |
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Best Local Similarity 100.0
Matches 317; Conservative
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                                                                                                                                GARIHINSWGAPVNGAYIIDSRNVDDYVRKNDMILLFAAGNEGPGSGIISAPGIAKNAII 180
                                                                                                                                                                       323 GARIHTINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT 382
                                                                                                                                                                                                                                                                181 VGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSFW 240
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                                       NANDPNGHGTHVAGSVLGNATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFSQAYSA 120
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73.2%; Score 1649; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.2e-126;
Matches 317; Conservative 0; Mismatches 0; Indels
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Sequence 10, Application US/09512251A

Parent No. 6555355

Parent No. 6555355

Parent No. 6555355

Parent InfoRMATION:
APPLICANT: Hansen, Peter
APPLICANT: Mikelsen, Frank
APPLICANT: Andersen, Kim
ITTLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5349:204-US
CURRENT FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 12

SCOFTWARE: Patentin Version 3.1

SEQ ID NO: 10

SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSGPORFSLAIVH 635
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                                                                                                                                                                                                                                                        29 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 88
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                                                                                                                                                                        0; Indels 0; Gaps
                                                                                                                     Query Match 73.2%; Score 1649; DB 4; Length 345; Best Local Similarity 100.0%; Pred. No. 6.2e-126; Matches 317; Conservative 0; Mismatches 0; Indels (
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Patent No. 6261822
Patent No. 6261822
Patent No. 6261822
Patent No. 6261822
Patent No. 626182
Patent No. 626182
Papel CANT: MORISHITA, Miso
Papel CANT: MITA, Masanori
APPLICANT: MITA, Masanori
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
STATE: B.C.
COUNTRY: United States of America
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APPLICATION NUMBER. PCT/JP96/03253
FILING DATE. 07.NOV-1996
PRICR APPLICATION DATA.
APPLICATION NUMBER. JP 323285/1995
FILING DATE. 12.DEC-1995
ATTOCNEY AGENT INFORMATION.
NAME: Browdy, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBER: US/08/894,818B
20-MAY-1998
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20
CLASSIFICATION:
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Bacillus
US-09-196-281-13
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US-08-894-818B-1
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145 IGADTVWNSLGYDGSGVVVAIVDTGIDAN-----HPDLKGKVIGWYDAVNGRSTPYDDQ 198
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APPLICANT: SHIMOJO, Tomoko,
APPLICANT: SHIMOJO, Tomoko,
APPLICANT: SHIMOJO, Tomoko,
APPLICANT: RATO, Ikunoshin
ITILE OF INVENTION: SYSTEM FOR EXPRPESSING HYPERTHERMOSTABLE
FILE REPERENCE: TAKAKURA-6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
FRIOR APPLICATION NUMBER: 151969/1997
PRIOR PILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 12
LENGTH: 659
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
19.2%; Score 432.5; DB 3; Length 659;
Best Local Similarity 30.7%; Pred. No. 7.2e-27;
Matches 134; Conservative 62; Mismatches 156; Indels 85;
REFERENCE/DOCKET NUMBER: TAKAKURA=1
TELECHMUNICATION INFORMATION;
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Sequence 12, Application US/09445472

Patent No. 6758726

GENERAL INFORMATION:
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) ORGANISM: Thermococcus celer
US-09-445-472-12
                                                                                                                                                                                             LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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365 TPINDYYTKASGTSMATPHVSGVGALILQAH------PSWTPDKVKTALIETADIVAP 416
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                                                                                       67 GHGTHVAGSVLG----NATNKGNAPQANLVFQSIM--DSGGGLGGLPANLQTLFSQAYSA 120
                                                                                                                                                              199 GHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKY 258
                                                                  8 VKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALY-ALGRTNNANDPN 66
Query Match
19.2%; Score 432.5; DB 4; Length 659;
Best Local Similarity 30.7%; Pred. No. 7.2e-27;
Matches 134; Conservative 62; Mismatches 156; Indels 85; Gaps
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Search completed: March 31, 2004, 16:11:57 Job time : 14.9892 secs

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1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60
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100.0%; Score 2260; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.5e-169;
Matches 433; Conservative 0; Mismatches 0;
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2260
1 NDVARGIVKADVAQNNYGLY......EVQAYNVPSGPQRFSLAIVH 433
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
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AAW50082
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AAY17088
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*

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Match Length DB
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Perfect score:
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Aaw24122 Pyrococcu Aaw34838 Hyperther Aaw34123 Pyrococcu Aaw34841 Hyperther Aaw34131 Procease. Abb19483 T. yonsei Abb19483 T. yonsei Abu07391 Porsign B Aaw1366 Fragment Aaw1366 Fragment Aaw1366 BphA-mel Aaw1367 Brotein e Aav3600 Procease Aav364124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aaw24124 Pyrococcu Aa	ENTS			protease protein fragment.	; bleaching; dishwasher.						to T, Araki H, Sumitomo N;		l in detergent compositions.		bes novel Bacillus sp. alkaline proteases useful in is, especially in laundry, bleaching or automatic. The novel proteases have an increased detergency \$. o prior art alkaline proteases (31 and 23\$). This fragment of the alkaline protease Ya from Bacillus 1029) described in the method of the invention	
AAW24122 AAW348139 AAW34129 AAW3481129 ABB09483 ABB09483 ABB01180 ABB01180 AAW1366 AAW1366 AAW1366 AAW1366 AAW1368 AAW34839 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24124 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AAW24 AA	ALIGNMENTS	433 AA.		9) alkaline	, laundry			÷.			Y, Sa		ases useful	English.	vel Bacillicially in novel proting art alka nent of the described	1
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44446666 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	-	083 AAM50083 AAM50083;	2-AUG-20	cillus	Alkaline	Bacillus	P1209233	9-MAY-2 2-NOV-2	2-NOV-2 2-APR-2	(KAOS ) K	Hatada Y, Okuda M,	WPI; 2002	New modif	Claim 5;	his i eterg ishwa 34 - equen	Sequence
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/note= "The enzyme is modifed by methoxypolethyleneglycol
molecules covalently attached to the N-terminal amino
group and to fourteen unspecified amino groups of lysine
residues present on the surface of the enzyme"
                                                                             120
                                                                                                                                                                                                       VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW 240
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                                   NDVARGIVKADVAQNNYGLYGQGQLVAVADTGLDTGRNDSSMHBAFRGKITALYALGRTN
                                                                                                                                                                                                                                                                                                                                  NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
                                                                             NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAMNA
                                                                                                                                          GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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                  NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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methoxypolethyleneglycol; mPEG; skin, hair care product; cosmetic;
lipstick; hair gel; sun oil; shampoo; hair dye; insect repellant.
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25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance; detergency improver,
                                                                                                                                  GARIHINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTARVAIT
                                                                                                                                                                                             ANYNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
                                                                                                                                                                                                                                                                                                                        YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV
                  NDVARGIVKADVAQNNYGLYGOGOVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                             NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                           NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                                                            GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
                                                                                                                                                                        VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
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99.4%; Score 2247; DB 2; Length 433;
Best Local Similarity 99.3%; Pred. No. 5.7e-168;
Matches 430; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA coding alkali-protease Ya enzyme - has good alkali and resistance and improves detergency.
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N-PSDB; AAQ27516.
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                                                           The present sequence represents the Bacillus lion Y protease. The invention claims for enzymes covalently modified on their surface by the attachment of a large number of small polymeric molecules, e.g. the attachment of a large number of small polymeric molecules, e.g. to polyethylene glycols (PEG). The polymeric molecules are coupled to the N-terminal amino group and the amino groups of lysine residues found on the Surface of the enzyme. In the example glycol, the lion Y protease was modified using methoxypolethyleneglycol (mPEG) as the polymeric molecule. The N-terminal amino group and the amino groups of the fourteen lysine of the surface present on the surface of the lion Y protease were modified. Modification of the enzymes increases the stability and/or reduces the sensitising potential (allergenicity) of the enzyme, without significantly reducing enzymesic activity. Also, using a large number of relatively small polymeric molecules, rather than a few very large ones, provides a more even effect with reduced activity loss. The modified enzymes are claimed to be useful as components of a wide range of skin and hair care products, e.g. soaps, cosmetics, oreams, gels, libsticks, but gels, sun oils, shampoos, hair dyse, insect repellants, etc
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skin and hair care products, has reduced tendency to cause sensitisation and increased stability.
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Pred. No. 5.7e-168;
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The sequence is that of Lion Y protease. This can be used as an active ingredient: (1) in personal care products (especially skin-care products such as soaps, cosmetics, hair dyes, sunscreens, anti-acne products, antiperspirants, insect repellants or decodorants); (ii) in detergents (as laundry, dishwashing or hard-surface cleaners); (iii) food or feed additives (e.g. for breadmaking); (iv) in textile-treating compositions, or (v) in oral or dermal pharmaceuticals and agrochemicals
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cosmetic; hair dye; sunscreen; acne; antiperspirants; insect repellant; deodorant; detergent; food; breadmaking; textile-treating; oral; dermal; pharmaceutical; agrochemical.
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Pred. No. 5.7e-168;
3; Mismatches 0;
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97US-0051830P.
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Best Local Similarity 99.3%;
Matches 430; Conservative
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NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA 120
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241 ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
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                                                                            301 NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
                                                                                                                                                                    361 YTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lion Y enzyme; protease; allergic response; industrial composition; co-polyme; ethylane oxide; B0; propylene oxide; P0; conjugate; allergenicity; detergent; cosmetic; totolerries; textile treatment; agrochemical; pharmaceutical; food; feed additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%; Score 2247; DB 3;
99.3%; Pred. No. 5.7e-168;
tive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an
in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New conjugate of polypeptide, especially ethylene oxide and propylene oxide, used has reduced allergenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 56~57; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44619 standard; protein; 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-DK000359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9BDK-00000809
                                                                                                                                                                                                                                                                                                   PSGPQRFSLAIVH 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus Lion Y enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olsen AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-136981/12.
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Best Local Similarity
Matches 430; Conserv
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                                                                                                                                                                                                                                                                     421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a protease Lion Y protein. The protein may be used to produce the conjugates of the invention. The specification describes polypeptide-polymer conjugates which have improved washing performance and reduced respiratory allergenicity compared with the unconjugated polypeptide. The polymer provides, in water, a conformation that shields the molecular surface effectively, preventing association of antibodies that can induce an allergic reaction. The conjugates are used in industrial compositions, particularly detergent formulations (laundry, dishwashing or hard surface cleaners), but also in agricultural chemicals, skin care products (cosmetics and toileries), oral and dental pharmaceuticals, or textile processing and treatment compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide-polymer conjugate, particularly enzyme conjugate, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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                                                                                                                                                                                                                                                                     Protease Lion Y; polypeptide-polymer conjugate; washing performance; respiratory allexgent formulation; laundry; dishwashing; hard surface cleaner; agricultural chemical; skin care; cosmettic; oral pharmaceutical; dental pharmaceutical;
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Pred. No. 5.7e-168;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deussen H,
                                                                                                                                                                                                                    Amino acid sequence of protease Lion Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 74-76; 79pp; English.
                                                                            AAY69207 standard; protein; 433 AA
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llarity 99.3%;
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Best Local Similarity
Matches 430; Conserv
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textile processing.
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                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus sp.
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                                                                                   VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW 240
                                                                                                                               ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP 300
                                                                                                                                                      NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS 360
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 NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA 120
                                  GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
                                                               VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
                                                                                                            ANYNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
                                                                                                                                                                                                                                                                                                                                                                                       (FERM BP-11162) alkaline protease protein fragment
                      GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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Pred. No. 2e-167;
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12-APR-2001; 2001JP-00114048.
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Saeki K;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV
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                                                                                               61 NANDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                                                                                                          181 VGATENYRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW
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                          1 NDVARGIVKADVAQNNYGLYGGGQVVAVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                NASDPNGHGTHVAGSVLGNALNKGNAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWNA
                                                                                                                                   GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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1 NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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           production of such proteases. The protease are used in laundry and dishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debittering and enhancing the degree of hydrolysis of protein hydrolysates, for flavour development through hydrolysis of proteins, degradation of undesired peptides and enzymatic synthesis of peptides. They have enhanced stability towards oxidation under alkaline conditions, e.g. towards bleaching agents of the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
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                                                                                                                                                                                  1; Indels
 recombinant host cells and methods for the
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                                                                                                                                                           Score 2238; DB 2,
Pred. No. 5e-167;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                            New modified alkaline proteases useful in detergent compositions
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                                        Sumitomo
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                        Ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein A-2 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2234; DB 5;
Pred. No. 6e-167;
3; Mismatches 3;
                                     Araki
                                        Ė
                                        Sato
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                                                                                                                                                                                     Claim 5; Page 13-15; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein; 433
                                        Kageyama
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Best Local Similarity 98.6%;

Matches 427; Conservative
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                                     Ogawa A,
Saeki K;
                                                                                                WPI; 2002-437518/47
(KAOS ) KAO CORP
                                                                                                                                                                                                                                                                                                                                                                              Sequence 433 AA;
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                                                            Okuda M,
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                                        Hatada
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209. .641
/note= "mature protein"
                                                                                         . .33
note= "signal peptide"
                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 53-54; 77pp; English
                                                                                                                                                                                                                                                                   (NOVO ) NOVO NORDISK BIOTECH INC.
                                                                                                                           note= "prepro
                                                                                                                                                                                                                     98WO-US012005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.77
Matches 384; Conservative
                                                                                                              .208
Bacillus JP170 protease
                                                                                                                                                                                                                                                                                        Christianson
                                                                                                                                                                                                                                                                                                             WPI; 1999-080908/07.
N-PSDB; AAV82382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 641 AA;
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                                                        Bacillus
                                                                               Key
Peptide
                                  flavour
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                                                                                                                                                                                                                     This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease A-2 from Bacillus sp NCIB12513 described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                       NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLFSNLNTLFSQAWNA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGIISAPGTAKNAIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW 240
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                                                                                                                                                                                                                                                                                                                                                                          1 NDVARGIVKADVAQNNYGLYGGGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60
                                                                                                                                                                                                                                                                                                                                                                                              1 NDVARGIVKADVAQNNFGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGDOGWGRUTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTLVNDLDLVITAPNGQKYVGNDFSYPYDNWWDGRNNVENVFINAPQSGTYIIEVQAYNV
                                                                                                                                                                         New modified alkaline proteases useful in detergent compositions
                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                  Sumitomo
                                                                                                                                                                                                                                                                                                                             Length 433;
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                                                                                                                                                                                                                                                                                                                            90.0%; Score 2033; DB 5; 88.7%; Pred. No. 3.8e-151; ive 25; Mismatches 24;
                                                                                                                 Araki
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                                                                                                                  Sato
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                                                                                                                                                                                               Claim 5; Page 20-21; 25pp; English
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                                                                                                                  Kageyama
                                  22-NOV-2001; 2001EP-00127851.
                                                         22-NOV-2000; 2000JP-00355166.
12-APR-2001; 2001JP-00114048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433
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                                                                                                                  Ogawa A,
Saeki K,
                                                                                                                                                    WPI; 2002-437518/47.
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                          (KAOS ) KAO CORP.
                                                                                                                                                                                                                                                                                                        Sequence 433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-1999
             29-MAY-2002
                                                                                                                 Hatada Y,
Okuɗa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW89547;
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ID AAW8
XX
AC AAW8
XX
DT 12-P
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This is the amino acid sequence of a novel protease of Bacillus sp. JP170 (NCIB 12513), as deduced from the nucleotide sequence of an isolated gene (see AAW82829. The entire protein, including the signal peptide and protein, and proteins and protease Y (see AAW8548) (Tom Bacillus. The invention provides vectors, recombinant host cells and methods for the recombinant production of the protease The protease is used in laundry and dishwashing detergents, for institutional and industrial cleaning, and for leather processing, as well as for debitering and enhancing the degree of hydrolysis of proteins, hydrolysates, for flavour development through hydrolysis of proteins, degradation of undesired peptides and in enzymatic synthesis of proteins, thas enhanced stability towards oxidation under alkaline conditions, cells, towards bleaching agents of the protease activity is diminished. Such provides mutent cells in which the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing.
Protease; detergent; surfactant; leather processing; debittering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              °,
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88.7%; Pred. No. 6.5e-151;
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This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease KP9860 from Bacillus sp strain KSM-KP9860 described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
181 TVGATENIRPSFGSYADNINHVAOFSSRGPTKDGRIKKPDVMAPGTFILGARSSLAPDSSF
                                                                                                         361 SVTLVNDLDLVITAPNGTKYVGNDFTAPYDNWMDGRNNVENVFINAPQSGTYTVEVQAXN
                                         TVGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF
                                                                                           WANYNSKYAYMGGISMAIPIVAGNVAQLREHFIKNRGIIPKPSLIKAALIAGAIDVGLGY
                                                                                                                                            PNGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTA
                                                                                                                                                                                               SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             protease; detergent; laundry; bleaching; dishwasher.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus ap KSM-KP9860 alkaline protease protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Araki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato T,
                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 12-13; 25pp; English
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                                                                                                                                                                                                                                                                                                                                            AAM50081 standard; protein; 434
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12-APR-2001; 2001JP-00114048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2001; 2001EP-00127851
                                                                                                                                                                                                                                                    VPSGPORFSLAIVH 433
                                                                                                                                                                                                                                                                  VPQGPQAFSLAIVN 434
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogawa A,
Saeki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-437518/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1209233-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel Bacillus sp. alkaline proteases useful in detergent compositions, especially in laundry, bleaching or automatic dishwasher detergents. The novel proteases have an increased detergency $ (34 - 38) compared to prior art alkaline proteases (31 and 23%). This sequence represents a fragment of the alkaline protease A-1 from Bacillus sp NCIB12289 described in the method of the invention
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                                                                                                         361 YILVNDLDLVITAPNGOKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV 420
     ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP 300
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                                                                      LTLVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYNV
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                      449 ANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGFP
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                                                                                                                                                                                                                                                                                                                                                          Alkaline protease; detergent; laundry; bleaching; dishwasher
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                                                                                                                                                                                                                                                                                                                               protein A-1 fragment.
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12-APR-2001; 2001JP-00114048
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Best Local Similarity 87.69
Matches 380; Conservative
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Saeki K;
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                                                                                                                                            AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMT1LFAAGNEGPNGGT1SAFGTAKNAI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is
                                                                                                                                                                                                              TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTYILSARSSLAPDSSF
                                      NASDPNGHGTHYVAGSVLGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN
                                                                        NANDTNGHGTHVAGSVLGNGATNKGMAPQANLVFQSIMDSSGGLGGLPSNLQTLFSQAFS
  NDVARGIVKADVAQSSYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                              AGARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAI
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(first entry)
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Nomura M;
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stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as erzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the enzyme to be an effective component of washing compositions including bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVILVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NASDPNGHGTHVAGSVLGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTYILSARSSLAPDSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 WANYNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY
                                                                                                                                                                                                                                                                                                                                                                                                              NDVARGIVKADVAQNNYGLYGQGQVVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
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composition, oxidising agent.
                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                   88.1%; Score 1991.5; DB 2; 87.8%; Pred. No. 1.2e-147; ive 27; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                             381; Conservative
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                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                        Sequence 639 AA;
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Kageyama Y;

Hitomi J,

Saeki K, Kubota H,

Okuda M, Nomura M;

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WPI; 1999-287736/27.
Takaiwa M,
Shikata S,
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The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by claicated and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the range 6-H 6-12; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-H, (c) its isoelectric point is 8.9-9.1, (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the bleaches. The present sequence represents an alkaline protease. (Updated on 20-MAR-2003 to correct DR field.) Alkali protease from Bacillus used in washing powders. Disclosure; Page 63-68; 71pp; Japanese. N-PSDB; AAX37279 

Sequence 640 AA;

266 61 NASDPNGHGTHVAGSVLGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN 119 1 NDVARGIVKADVAQNNYGLYGQGQVVAVAVATGLDTGRNDSSMHBAFRGKITALYALGRTN 60 NDVARGIVKADVAQSSYGLYGOGOIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN Gaps 1, Query Match
Best Local Similarity 87.3%; Pred. No. 2e-147;
Matches 379; Conservative 29; Mismatches 25; Indels 1; 원 à

180 TVGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSF 239

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567 SVTLVNDLDLVITAPNGTQYVGNDFTSPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 626

Search completed: March 31, 2004, 16:04:31 Job time: 48.1304 secs

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ADDRESSEE: No. 63037520 No. 6303752disk of No. 6303752th America, Inc. STREET: 405 Lexington Avenue CITY: New York STATE: NY COUNTRY: NY ZEPATE: NY COUNTRY: USA ZIP: 10174
                      8, Appli
6, Appli
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99.4%; Score 2247; DB 4; Length 433;
Best Local Similarity 99.3%; Pred. No. 4.4e-169;
Matches 430; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER RADABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,623A
FILING DATE: 25-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: ROZEK, CAPO, 18,993
REGISTRATION NUMBER: 36,993
REGISTRATION NUMBER: 36,993
REGISTRATION NUMBER: 5256.200-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-013
TELEPHONE: 212-867-013
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TELEPHONE: 213-867-013
TELEPHONE: 213-865-5
TEMPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                    US-08-694-8188-8
US-08-445-472-6
US-08-750-406A-1
US-08-750-406A-1
US-08-37-118-1
US-08-431-387-5
US-08-431-387-6
US-08-322-677A-10
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US-08-325-677A-10
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US-08-88-218-10
US-08-88-218-10
US-08-88-218-10
US-08-88-218-10
                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09104623A
Patent No. 6303752
GENERAL INFORMATION:
APPLICANT: Olsen, Arne Agerlin
APPLICANT: Fatum, Time Muxch!
APPLICANT: Patum, Heinz-Josef
APPLICANT: Roussen, Heinz-Josef
APPLICANT: Roggen, Heinz-Josef
APPLICANT: Roggen, Erwin Ludo
TITLE OF INVENTION: A Modified Polypeptide
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   US-09-024-532-3
US-08-269-050-4
US-08-090-207-1
                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 433 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE: STRAIN: Bacillus sn.
linear
TOPOLOGY:
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Sequence 42, Appl
Sequence 8, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 10, Appli
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Sequence 4, Appli
                                                                                     March 31, 2004, 15:59:39; Search time 13.9892 Seconds (without alignments) 1597.947 Million cell updates/sec
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2260
1 NDVARGIVKADVAQNNYGLY.......EVQAYNVPSGPQRFSLAIVH 433
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Sequence 8
Sequence 6
Sequence 1
Sequence 2
Sequence 1
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1. /GgnZ_6/ptodatca/2/jaa/5A_COMB.pep:*

2. /GgnZ_6/ptodatca/2/jaa/5B_COMB.pep:*

3: /cgnZ_6/ptodatca/2/jaa/6A_COMB.pep:*

4: /cgnZ_6/ptodatca/2/jaa/BECOMB.pep:*

5: /GgnZ_6/ptodatca/2/jaa/PCTUS_COMB.pep:*

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6: /cgnZ_6/ptodatca/2/jaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-138-746-4

US-08-873-479-43

US-08-873-479-43

US-09-509-814A-4

US-09-509-814A-6

US-09-509-814A-6

US-09-509-814A-1

US-09-509-814A-1

US-09-512-251A-10

US-09-512-251A-10

US-09-512-251A-10

US-09-512-251A-10

US-09-618-113

US-09-618-113

US-09-645-472-12

US-09-645-472-12

US-09-645-472-12

US-09-645-472-12

US-09-645-472-12

US-09-645-472-13

US-09-645-472-13

US-09-645-472-14

US-09-645-472-14
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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US-09-000-016-7
US-09-514-340-7
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Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
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Match Length DB
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22247
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Sequence:
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No.
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360 420 420

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61 NASDPNGHGTHVAGSVLGNALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAMNA 120
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121 GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT 180
                                                                                                                               241 ANYNSKYAYMGGISMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP 300
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                                                                      NGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTAS
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99.4%; Score 2247; DB 4;
Best Local Similarity 99.3%; Pred. No. 4.4e-169;
Matches 430; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09338746;
Patent No. 6638526;
GENERAL INFORMATION:
APPLICANT: Deussen, Heitz-Josef
APPLICANT: Olsen, Arne A.
APPLICANT: Roggen, Erwin L.
TITLE OF INVENTION: A POlypeptide-Polymer Con
FILE REFERENCE: 5612.00-US;
CURRENT PELING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: WS/09/338,746
CURRENT FILING DATE: 1999-06-23
EARLIER FILING DATE: 1988-06-23
EARLIER FILING DATE: 1988-06-33
EARLIER FILING DATE: 1988-06-33
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EARLIER FILING DATE: 1988-06-33
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; ORGANISM: Bacillus
US-09-338-746-4
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                       1 NDVARGIVKADVAQNNYGLYGQGQLVAVADIGLDIGRNDSSMHEAFRGKITALYALGRIN
                                                                                                                                                                                              GARIHTINSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT
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99.4%; Score 2247; DB 4;
Best Local Similarity 99.3%; Pred. No. 4.4e-169;
Matches 430; Conservative 3; Mismatches 0;
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APPLICANT: Olsen, Arnette
TITLE OE INVENTION:
TITLE REFERENCE: 4922.204 US
CURRENT APPLICATION NUMBER: US/09/019,532B
CURRENT APPLICATION NUMBER: US/09/019,532B
CURRENT FILING DATE: 1997-01-10
EARLIER PPLICATION NUMBER: 0784/97
EARLIER APPLICATION NUMBER: 0784/97
EARLIER PLING DATE: 1997-06-25
EARLIER PLING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1997-07-07
SARLIER FILING DATE: 1998-01-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASSEQ for Windows Version 3.0
SERICHH: 433
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ORGANISM: Bacillus sp.
-09-019-532-4
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US-09-019-532-4
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                                                      443 ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
APPLICANT: Lynne, Christianson
TITLE OF INVENTION: Macleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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88.7%; Pred. No. 5.5e-152;
iive 25; Mismatches 24;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OFFRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFICATION: 530
ATTORNALPOCKENT UNIBER: 34,086
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELEPHONE: 212-867,0123
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CITY: New York
STATE: NY
COUNTRY: USA
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Matches 384; Conservative
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INFORMATION FOR SEQ ID NO:
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FRAGMENT TYPE: internal
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STRANDEDNESS: si
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US-08-873-479-42
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SGDQGWGRVTLDXSLNVAYVNEATALATGQXATYSFQAQAGKPLXISLVWTDAPGSTTAS 360
                                                                                                   361 YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV 420
                                                                       YILVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYNV 420
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99.4%; Score 2247; DB 2; Length 635;
Best Local Similarity 99.3%; Pred. No. 7.5e-169;
Matches 430; Conservative 3; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sloma, Alan
APPLICANT: Slome, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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ZIF: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: IZ-JUN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: AGI'S: Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/08873479 Patent No. 5891701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 635 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                   421 PSGPORFSLAIVH 433
                                                                                                                                                                                                           421 PSGPORFSLAIVH 433
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linear
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61 NASDPNGHGTHVAGSVLGN-ALNKGMAPQANLVFQSIMDSSGGLGGLPSNLNTLFSQAWN 119
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386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTYILSARSSLAPDSSF 445
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                                                                                                                                                                                                                                                                               360 SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYN
                                                                                                                                                                                                                                                                                                                  SVTLVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN
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                                                                                           300 PNGDQGWGRVTLNKSLNVAYVNEATALATGQKATYSFQAQAGKPLKISLVWTDAPGSTTA
                                                             240 WANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKNRGITPKPSLIKAALIAGATDVGLGY
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88.0%; Score 1988.5; DB 4

Best Local Similarity 87.3%; Pred. No. 1.7e-148;

Matches 379; Conservative 29; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-509-104-104-10

Sequence 8, Application US/09509814A

Patent No. 637627

GENERAL INFORMATION:
APPLICANT: TAKATWA, MITSUYOSHI
APPLICANT: SAEKT, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: SHIKATA, SAINSUW
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; TYPE: PRT
; ORGANISM: Bacillus Sp.
US-09-509-814A-8
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                                                                                                                                             VGATENYRPSFGSIADNPNHIAQFSSRGATRDGRIKPDVTAPGTFILSARSSLAPDSSFW 240
                                                                                                                                                                             ANYNSKYAYMGGTSMATPIVAGNVAQLREHFIKWRGITPKPSLIKAALIAGATDVGLGYP 300
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                                                                            GARIHINSWGAPVNGAYIIDSRNVDDYVRKNDMIILFAAGNEGPGSGIISAPGIAKNAIT 388
                                   GARIHTNSWGAPVNGAYTANSRQVDEYVRNNDMTVLFAAGNEGPNSGTISAPGTAKNAIT 180
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GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: SAEKI, KATSUHISA
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBCA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: HATOMI, JUN
APPLICANT: SHIKATA, SHIRGUM
APPLICANT: SHIKATA, SHIRGUM
APPLICANT: SHIKATA, SHIRGUM
APPLICANT: MAGENAMI
APPLICANT: NOWURA, MASATUMI
ITILE OF INVENTION: ALKALINE PROTEASE
FILE REPERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VEISION 3.0
SOFTWARE: PATENTIN VEISION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09509814A Patent No. 6376227 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 PVSPOTFSLAIVH 641
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ORGANISM: Bacillus sp.
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APPLICANT: HITOMI, JUN
APPLICANT: HITOMI, JUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUM
APPLICANT: NOWURA, MASARUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 032-0632-09CT
CURRENT APPLICATION NUMBER: UCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR PRILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
SEQ ID NOS: 24
SOCTWARRE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 639
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OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (89)...(89)
OTHER INPORMATION: Xaa
NAME/KEY: misc_feature
LOCATION: (102)...(102)
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (105)...(105)
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (128)...(128)
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (128)...(128)
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (128)...(128)
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (130)...(130)
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LOCATION: (23). (23)
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NAME/KEY: misc_feature
LOCATION: (29). (29)
LOCATION: (29). (29)
LOCATION: (29). (29)
NAME/KEY: misc_feature
LOCATION: (23). (23)
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LOCATION: (23). (23)
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (47)...(47)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (53)...(53)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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THER INFORMATION: Xaa is any amino acid
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420 VPSGPORFSLAIVH 433
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APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
                                                              627 VPVGPOTFSLAIVN 640
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SYTLVNDLDLVITAPNGQKYVGNDFSYPYDNNWDGRNNVENVFINAPQSGTYIIEVQAYN 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-509-814A-6

US-09-509-814A-6

Sequence (A. Application US/09509814A

Patent No. 6376227

GENERAL INFORMATION:

APPLICANT: TAKAINA, MITSUYOSHI

APPLICANT: SAEKI, KATSUHISA

APPLICANT: KAGEYAMA, YASUSHI

APPLICANT: HITOMI, JUN

APPLICANT: HITOMI, JUN

APPLICANT: HITOMI, AUN

APPLICANT: HATOMI, AUN

APPLICANT: HATOMI, AUN

APPLICANT: HATOMI, AUSAFUMI

ITILE OF INVENTION: ALKALINE PROTEASE

FILE REFERENCE: 0327-0832-0PCT

CURRENT FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: US/09/509,814A

CURRENT FILING DATE: 1997-06-08

PRIOR APPLICATION NUMBER: UF 9-274570

PRIOR FILING DATE: 1997-06-08

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTH NUMBER: UF 9-274570

PRIOR FILING DATE: 1997-06-08

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTH NUMBER: UF 9-274570

PRIOR FILING DATE: 1997-06-08

SEQ ID NO 6

LENGTH 640

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; ORGANISM: Bacillus sp.
US-09-509-814A-6
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LOCATION: (131)(131) OTHER INFORMATION: Xaa i. NAME/KEY. migg feature	OCHER INFORMATION: Xaa i	OCHER INCRATION: Xaa i	NAME/AEI: MISC LEACUTE LOCATION: (146) OTHER INFORMATION: Xaa i	NAME/KEY: misc feature LOCATION: (148)(148)	OTHER INFORMATION: Xaa i NAME/KEY: misc feature	LOCATION: (160)(160) OTHER INFORMATION: Xaa i NAME/KEY: misc feature	LOCATION: (165)(165) OTHER INFORMATION: Xaa i	NAME/KEY: misc feature LOCATION: (172)(172)	OTHER INFORMATION: Xaa i NAME/KEY: misc_feature	LOCATION: (183)(183) OTHER INFORMATION: Xaa i	LOCATION: (187)(187) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (188)	NAME/KEY: misc feature	CONTION: (189) (189) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (194)(194)	NAME/KEY: misc feature	OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (306)(306)	OTHER INFORMATION: Xaa : NAME/KEY: misc feature :OCAMIOM: (2247 (224)	OTHER INFORMATION: Xaa :	LOCATION: (369) (369)	OTHER INFORMATION: Add NAME/KEY: misc feature	OTHER INFORMATION: Xaa	LOCATION: (501)(501) OTHER INFORMATION: Xaa	NAME/KEY: misc feature LOCATION: (531)(531)	OTHER INFORMATION: Xaa NAME/KEY: misc feature	(541)(541) DRMATION: Xaa	: "		0 ~ a	NAME/KEY: misc feature LOCATION: (594)(594)

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                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                          Query Match 85.9%; Score 1941.5; DB 4; Length 639; Best Local Similarity 86.2%; Pred. No. 8.8e-145; Matches 374; Conservative 21; Mismatches 38; Indels 1;
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APPLICANT TAKAIWA, MIXIO
APPLICANT SAKUKA, MIXIO
APPLICANT SAKUA, MIXIO
APPLICANT SAKUKA, KATSUHISA
APPLICANT SAKUK, KATSUHISA
APPLICANT HITOMI, JUN
APPLICANT SHIKATA, SHITSUW
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APPLICANT SHIKATA, SHITSUW
APPLICANT NOWINA, MASAFUM
CURRENY APPLICATION NUMBER: US/09/509,814A
CURRENY FILING DATE: 2000-04-06
PRIOR PILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1997-06-08
OTHER INFORMATION: Kaa is any amino acid
INAME/KEY: misc feature
LOCATION: (595)...(595)
OTHER INFORMATION: Kaa is any amino acid
NAME/KEY: misc feature
LOCATION: (596)...(596)
OTHER INFORMATION: Kaa is any amino acid
NAME/KEY: misc feature
LOCATION: (611)...(611)
OTHER INFORMATION: Xaa is any amino acid
LOCATION: (611)...(611)
OTHER INFORMATION: Xaa is any amino acid
LOCATION: (632)...(632)
COTHER INFORMATION: Xaa is any amino acid
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Sequence 2, Application US/09509814A
Patent No. 6376227
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